

GenCore version 5.1.6
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M protein - protein search, using sw model

Run on: November 21, 2003, 15:19:18 ; Search time 58.8082 Seconds
(without alignments)
286.100 Million cell updates/sec

Title: US-09-010-377-1

Percent score: 562
Sequence: 1 DIQMTQSPSSLSASVGRVT.....YCLQDNLMTFGQGTKEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	562	100.0	106	AA1981321	Humanized anti-VLA
2	562	100.0	106	AA1982412	Humanised alpha-4
3	562	100.0	126	AA1982419	Humanised alpha-4
4	508	90.4	106	AA1981328	Mouse anti-VLA-4 a
5	508	90.4	126	AA1981326	Mouse VLA-4 antibo
6	508	90.4	126	AA1981332	Human VLA-4 reshap
7	508	90.4	126	AA1982409	Alpha-4 integrin m
8	488	85.8	359	AA1982913	Human MCP-3 and mu
9	488	85.8	361	AA1982911	Human IP-10 and mu

10	488	86.8	374	20	AA1982916	Artificial synthe
11	481	85.6	128	15	AA1980627	ME1-14 light chain
12	475.5	84.6	234	15	AA19813050	CD4-specific CDR-9
13	471.5	83.9	107	16	AA19878970	Light chain variab
14	465	82.7	108	17	AA1983159	Murine monoclonal
15	460.5	81.9	128	11	AA19806252	Variable region of
16	460	81.9	637	13	AA19826983	(FRP51)-ETA fusion
17	456	81.1	109	19	AA19826797	Anti-gp54 MAb T16
18	455	81.0	240	16	AA1985495	SCF(FWP51). Sync
19	455	81.0	241	20	AA19821882	Amino acid sequenc
20	455	81.0	245	19	AA19826800	Anti-gp54 MAb T16
21	453.5	80.7	107	16	AA1981322	Humanized VLA-4 an
22	453.5	80.7	107	18	AA19822422	Humanised alpha-4
23	453	80.6	109	12	AA19813658	Murine OKT4A light
24	452	80.4	241	13	AA19826981	FWP51 fusion prote
25	451.5	80.3	108	16	AA1985163	Human REI monoclon
26	451.5	80.3	129	15	AA19847207	Human/murine IL-1
27	451	80.2	355	18	AA19835133	R. pipiens recombi
28	449.5	80.0	107	19	AA1986805	Variable light dom
29	449.5	80.0	107	19	AA19870825	Humanised murine a
30	449.5	80.0	107	23	AA19811194	Humanised anti-VEG
31	446.5	79.4	108	18	AA19810231	CDR-grafted light
32	446.5	79.4	110	19	AA19870673	Anti-VEGF humanise
33	446.5	79.4	110	23	AA19861242	Humanised anti-VEG
34	446.5	79.4	234	18	AA19810233	TF8-5G9 CDR-grafte
35	446.5	79.4	237	19	AA19870703	Protein encoded by
36	446.5	79.4	650	23	AA19811341	Phage-display anti
37	445.5	79.3	107	19	AA1986804	Variable light dom
38	445.5	79.3	107	19	AA19870623	Humanised murine a
39	445.5	79.3	107	23	AA19811192	Humanised anti-VEG
40	444.5	79.1	107	20	AA1987455	Humanised anti-alp
41	444.5	79.1	107	22	AA19862087	Human VI consensus
42	444.5	79.1	107	22	AA19860400	Consensus human I
43	444.5	79.1	107	22	AA19861585	Human variable lig
44	444.5	79.1	108	19	AA19870622	Human consensus fr
45	444.5	79.1	108	21	AA1982345	Human consensus se

ALIGNMENTS

RESULT 1
AA1981321
ID AA1981321 standard; Protein; 106 AA.
XX
AC AA1981321;
XX
DT 02-APR-1996 (first entry)
XX
DE Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
XX
OS antibody engineering.
XX
OS Chimeric Mus musculus.
XX
OS Chimeric Homo sapiens.
XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
(ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
leukocyte adhesion to endothelial cells, partic. for treating

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protein - protein search, using sw model

on: November 21, 2003, 15:21:54 ; Search time 19.9658 Seconds
(without alignments)
224.632 Million cell updates/sec

le: US-09-010-377-1

fect score: 562

uence: 1 DIQWTQSPSLASVGRVT.....YCLQYDNLWTFQGTQKVEIK 106

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

rchd: 328717 seqs, 42310858 residues

al number of hits satisfying chosen parameters: 328717

imum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
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- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
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2	562	100.0	106	5	PCT-US95-01219-7	Sequence 7, Appl
3	508	90.4	106	2	US-08-561-521-5	Sequence 5, Appl
4	508	90.4	106	5	PCT-US95-01219-5	Sequence 5, Appl
5	508	90.4	126	2	US-08-561-521-2	Sequence 2, Appl
6	508	90.4	126	2	US-08-561-521-15	Sequence 15, Appl
7	508	90.4	126	5	PCT-US95-01219-2	Sequence 2, Appl
8	508	90.4	126	5	PCT-US95-01219-15	Sequence 15, Appl
9	488	86.8	359	4	US-09-646-028-16	Sequence 16, Appl
10	488	86.8	361	4	US-09-646-028-13	Sequence 13, Appl
11	488	86.8	374	4	US-09-646-028-15	Sequence 15, Appl
12	481	85.6	128	1	US-08-339-582-4	Sequence 4, Appl
13	471.5	83.9	107	2	US-08-898-366-22	Sequence 22, Appl
14	460	81.9	637	1	US-08-235-938-16	Sequence 16, Appl
15	460	81.9	637	2	US-08-465-473B-16	Sequence 16, Appl
16	455	81.0	241	1	US-08-235-838-11	Sequence 11, Appl
17	455	81.0	241	2	US-08-465-473B-11	Sequence 11, Appl
18	454.5	80.9	108	2	US-08-602-725-29	Sequence 29, Appl
19	453.5	80.7	107	2	US-08-561-521-8	Sequence 8, Appl
20	453.5	80.7	107	5	PCT-US95-01219-8	Sequence 8, Appl
21	451	80.2	355	3	US-08-875-811-57	Sequence 57, Appl
22	448.5	79.8	107	2	US-07-934-373C-17	Sequence 17, Appl
23	448.5	79.8	107	3	US-08-437-642B-17	Sequence 17, Appl
24	448.5	79.8	107	4	US-08-146-206C-17	Sequence 17, Appl
25	448.5	79.8	107	5	PCT-US93-07832-17	Sequence 17, Appl
26	444.5	79.1	107	2	US-07-934-373C-18	Sequence 18, Appl
27	444.5	79.1	107	3	US-08-437-642B-18	Sequence 18, Appl

28 444.5 79.1 107 4 US-08-146-206C-18 Sequence 18, Appl
29 444.5 79.1 107 5 PCT-US93-07832-18 Sequence 18, Appl
30 444.5 79.1 108 3 US-08-974-893-3 Sequence 3, Appl
31 444.5 79.1 111 1 US-08-137-117D-67 Sequence 67, Appl
32 444.5 79.1 111 2 US-08-436-717-67 Sequence 67, Appl
33 444.5 79.1 126 1 US-08-137-117D-71 Sequence 71, Appl
34 444.5 79.1 126 2 US-08-436-717-71 Sequence 71, Appl
35 443.5 78.9 107 2 US-08-561-521-6 Sequence 6, Appl
36 443.5 78.9 107 2 US-08-652-558-34 Sequence 34, Appl
37 443.5 78.9 107 4 US-09-025-203-15 Sequence 15, Appl
38 443.5 78.9 107 5 PCT-US95-01219-6 Sequence 6, Appl
39 443.5 78.9 108 2 US-08-070-116A-7 Sequence 7, Appl
40 443.5 78.9 108 2 US-08-116-247-9 Sequence 9, Appl
41 443.5 78.9 108 4 US-08-557-050-7 Sequence 7, Appl
42 441.5 78.6 107 2 US-08-318-157B-6 Sequence 6, Appl
43 440.5 78.4 107 2 US-08-652-558-2 Sequence 2, Appl
44 440.5 78.4 109 2 US-07-934-373C-3 Sequence 3, Appl
45 440.5 78.4 109 3 US-08-437-642B-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-561-521-7
; Sequence 7, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-7

Query Match 100.0%; Score 562; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.6e-45;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DIQMTQSPSSLSASVGDRTVITCKTSQDINKYMAWYQQTGKAPRLLIHYTSALQPGIPS 60
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61 RFGSGSGRDYFTTISLQPEDATYYCLOYDNLWTFGGQTKVEIK 106
61 RFGSGSGRDYFTTISLQPEDATYYCLOYDNLWTFGGQTKVEIK 106

RESULT 2

CT-US95-01219-7

Sequence 7, Application PC/TUS9501219

GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

CT-US95-01219-7

Query Match 100.0%; Score 562; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.6e-45;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DIQMTQSPSSLSASVGDRTVITCKTSQDINKYMAWYQQTGKAPRLLIHYTSALQPGIPS 60
1 DIQMTQSPSSLSASVGDRTVITCKTSQDINKYMAWYQQTGKAPRLLIHYTSALQPGIPS 60
61 RFGSGSGRDYFTTISLQPEDATYYCLOYDNLWTFGGQTKVEIK 106
61 RFGSGSGRDYFTTISLQPEDATYYCLOYDNLWTFGGQTKVEIK 106

RESULT 3

S-08-561-521-5

Sequence 5, Application US/08561521

Patent No. 5840299

CT-US95-01219-7

Sequence 5, Application PC/TUS9501219

GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.

APPLICANT: Leger, Olivier J.

APPLICANT: Saldanha, Jose

APPLICANT: Jones, S. Tarran

TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

TITLE OF INVENTION: Adhesion Molecule VLA-4

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15270-14

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600

TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-561-521-5

Query Match 90.4%; Score 508; DB 2; Length 106;
Best Local Similarity 88.7%; Pred. No. 1.7e-40;
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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1 DIQMTQSPSSLSASVGDRTVITCKTSQDINKYMAWYQQTGKAPRLLIHYTSALQPGIPS 60

61 RFGSGSGRDYFTTISLQPEDATYYCLOYDNLWTFGGQTKVEIK 106

61 RFGSGSGRDYFTTISLQPEDATYYCLOYDNLWTFGGQTKVEIK 106

RESULT 4

PCT-US95-01219-5

Sequence 5, Application PC/TUS9501219

GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.

APPLICANT: Leger, Olivier J.

APPLICANT: Saldanha, Jose

APPLICANT: Jones, S. Tarran

TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

TITLE OF INVENTION: Adhesion Molecule VLA-4

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: November 21, 2003, 15:27:54 ; Search time 39.5685 Seconds
(without alignments)
489.058 Million cell updates/sec

Title: US-09-010-377-1

Perfect score: 562

Sequence: 1 DIQWTSQSSLSASVGRVT.....YCLQYDNLWTFGQTKVEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488	86.8	359	12	US-10-335-394-16
2	488	86.8	361	12	US-10-335-394-13
3	488	86.8	374	12	US-10-335-394-15
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6	466.5	83.0	108	9	US-09-229-200A-16
7	449.5	80.0	107	9	US-09-056-160B-15
8	449.5	80.0	107	12	US-10-234-671-15
9	446.5	79.4	110	9	US-09-056-160B-103
10	446.5	79.4	110	12	US-10-234-671-101
11	446.5	79.4	237	9	US-09-056-160B-100
12	446.5	79.4	237	12	US-10-234-671-100
13	446.5	79.4	491	14	US-10-011-125-2
14	445.5	79.3	107	9	US-09-056-160B-13
15	445.5	79.3	107	12	US-10-234-671-13

16	444.5	79.1	107	12	US-10-223-880-15	Sequence 15, Appl
17	444.5	79.1	107	15	US-10-268-501-5	Sequence 5, Appl
18	444.5	79.1	108	9	US-09-056-160B-12	Sequence 12, Appl
19	444.5	79.1	108	12	US-10-234-671-12	Sequence 12, Appl
20	444.5	79.1	108	12	US-09-795-798-3	Sequence 3, Appl
21	444.5	79.1	109	9	US-09-811-123-6	Sequence 6, Appl
22	444.5	79.1	110	12	US-10-044-896-4	Sequence 4, Appl
23	443.5	78.9	107	10	US-09-999-025-15	Sequence 15, Appl
24	443.5	78.9	107	10	US-09-999-040-15	Sequence 15, Appl
25	443.5	78.9	107	11	US-09-998-817-15	Sequence 15, Appl
26	443.5	78.9	107	11	US-09-999-021-15	Sequence 15, Appl
27	443.5	78.9	107	15	US-10-040-997-15	Sequence 15, Appl
28	443.5	78.9	108	9	US-09-229-200A-14	Sequence 14, Appl
29	443.5	78.9	108	12	US-10-428-662-100	Sequence 100, App
30	443.5	78.9	108	12	US-10-422-049-7	Sequence 7, Appl
31	443.5	78.9	108	15	US-10-267-286A-7	Sequence 7, Appl
32	443.5	78.9	110	9	US-09-056-160B-105	Sequence 105, App
33	443.5	78.9	110	12	US-10-234-671-103	Sequence 103, App
34	443	78.8	109	9	US-09-229-200A-7	Sequence 7, Appl
35	442.5	78.7	108	9	US-09-056-160B-8	Sequence 8, Appl
36	442.5	78.7	108	14	US-10-153-159-2	Sequence 2, Appl
37	442.5	78.7	108	14	US-10-153-159-16	Sequence 16, Appl
38	442.5	78.7	108	15	US-10-153-176-2	Sequence 2, Appl
39	442.5	78.7	108	15	US-10-153-176-16	Sequence 16, Appl
40	442.5	78.7	110	12	US-10-234-671-8	Sequence 8, Appl
41	442.5	78.7	131	15	US-10-207-655-256	Sequence 256, App
42	442.5	78.7	266	15	US-10-207-655-260	Sequence 260, App
43	442.5	78.7	550	15	US-10-207-655-270	Sequence 270, App
44	441.5	78.6	107	9	US-09-253-794-6	Sequence 6, Appl
45	439.5	78.2	108	14	US-10-153-159-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-10-335-394-16
; Sequence 16, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Bitagyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-16

Query Match 86.8%; Score 488; DB 12; Length 359;
Best Local Similarity 84.9%; Pred. No. 6.8e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQWTSQSSLSASVGRVTITCKTSQDINKYMWYQQTGKAPRLLIHYTSALOPGIPS 60
233 DIQWTSQSSLSASVGRVTITCKTSQDINKYMWYQQTGKAPRLLIHYTSALOPGIPS 292
QY 61 RFSGSGSGRDYFTFTISSLPEDIATYCIQYDNLWTFGQTKVEIK 106
293 RFSGSGSGRDYFTFTISSLPEDIATYCIQYDNLWTFGQTKVEIK 338

```
RESULT 2
US-10-335-394-13
; Sequence 13, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-13
Query Match      86.8%; Score 488; DB 12; Length 361;
Best Local Similarity 84.9%; Pred. No. 6.8e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy      1 DIQMTQSPSSLSASVGRVITCKTSQDINKYMWYQQTGKAPRLLIHYTSLALQPGIPS 60
Db      235 DIQMTQSPSSLSASLGKVIITCKASQDINKYIAWYQHKGPRLLIHYTSLALQPGIPS 294

Qy      61 RFSGSGGRDYTFITSSLPEDIAITYCYLDNLTWFGQGTKEIK 106
Db      295 RFSGSGGRDYTFITSSLPEDIAITYCYLDNLTWFGQGTKEIK 340

RESULT 3
US-10-335-394-15
; Sequence 15, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-15
Query Match      86.8%; Score 488; DB 12; Length 374;
Best Local Similarity 84.9%; Pred. No. 7.1e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy      1 DIQMTQSPSSLSASVGRVITCKTSQDINKYMWYQQTGKAPRLLIHYTSLALQPGIPS 60
Db      95 DIQMTQSPSSLSASLGKVIITCKASQDINKYIAWYQHKGPRLLIHYTSLALQPGIPS 154
```

```
Qy      61 RFSGSGGRDYTFITSSLPEDIAITYCYLDNLTWFGQGTKEIK 106
Db      155 RFSGSGGRDYTFITSSLPEDIAITYCYLDNLTWFGQGTKEIK 200

RESULT 4
US-09-229-200A-11
; Sequence 11, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
; APPLICANT: Jolliffe et al.
; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/229,200A
; FILING DATE: 13-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Wallen, III
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: ORT-948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 784-3239
; TELEFAX: (908) 524-2808
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 108
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-229-200A-11
Query Match      85.3%; Score 479.5; DB 9; Length 108;
Best Local Similarity 85.8%; Pred. No. 1.2e-36;
Matches 91; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy      1 DIQMTQSPSSLSASVGRVITCKTSQDINKYMWYQQTGKAPRLLIHYTSLALQPGIPS 60
Db      1 DIQMTQSPSSLSASVGRVITCKASPDINNLNLYQQTGKAPRLLIHYTSLALQPGIPS 60

Qy      61 RFSGSGGRDYTFITSSLPEDIAITYCYLDNLTWFGQGTKEIK 105
Db      61 RFSGSGGRDYTFITSSLPEDIAITYCYLDNLTWFGQGTKEIK 106

RESULT 5
US-09-229-200A-15
; Sequence 15, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
; APPLICANT: Jolliffe et al.
; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
```

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MM protein - protein search, using sw model

Run on: November 21, 2003, 15:21:14 ; Search time 19.6027 Seconds
(without alignments)
520.023 Million cell updates/sec

Title: US-09-010-377-1

Perfect score: 562

Sequence: 1 DIQMTQSPSSLSASVGRVT.....YCLQYDNLWTFGGTKVEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488	86.8	104	2	S26330
2	479	85.2	104	2	S26329
3	478	85.1	106	2	C39316
4	463.5	82.5	125	2	S03565
5	452	80.4	97	2	PH1064
6	446.5	79.4	107	2	PL0270
7	443.5	78.9	108	1	K1HURE
8	443.5	78.9	129	2	S52789
9	443	78.8	103	2	S26332
10	440.5	78.4	107	2	PL0272
11	440	78.3	94	2	E33730
12	439.5	78.2	107	2	PL0269
13	439.5	78.2	107	2	PL0271
14	439.5	78.2	108	1	K1HUAU
15	435.5	77.5	108	2	I39154
16	429.5	76.4	110	2	S44118
17	429.5	76.4	127	2	S40367
18	426	75.8	107	2	S36275
19	424.5	75.5	125	2	S40333
20	421.5	75.0	108	1	K1HULY
21	419.5	74.6	108	1	K1HUGY
22	419.5	74.5	123	2	S40331
23	418.5	74.5	109	2	S31998
24	415.5	73.9	109	2	S40352
25	414.5	73.8	131	2	S40352
26	414	73.7	124	2	S40336
27	413.5	73.6	108	1	K1HUSW
28	412.5	73.4	108	2	B49047
29	412	73.3	106	2	PC2397

30 410.5 73.0 108 2 S44122
31 410.5 73.0 109 2 S31981
32 409.5 72.9 129 1 K1HUKK
33 409 72.8 107 1 K1HUAR
34 408.5 72.7 108 1 K1HUWE
35 408.5 72.7 139 2 S40365
36 407.5 72.5 141 2 A49134
37 405.5 72.2 117 2 S46371
38 405 72.1 108 2 S30521
39 404.5 72.0 132 2 S40334
40 403.5 71.8 94 2 PH1063
41 403.5 71.8 107 2 S36264
42 403.5 71.8 127 2 S11240
43 403 71.7 117 2 S43528
44 403 71.7 117 2 S42263
45 402.5 71.6 108 1 K1HUUH

ALIGNMENTS

RESULT 1

S26330

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26330

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein ei
A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26330

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-104 <STA>

A:CROSS-references: EMBL:X59185; NID:G52316; PIDN:CAA41895.1; PID:gl334063

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 488; DB 2; Length 104;
Best Local Similarity 85.6%; Pred. No. 1.6e-35;
Matches 89; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCTQSDINKYMWYQOTPGKAPRLLIHYTSALQGPIS 60

Db 1 DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPELLIHYTSTLQGPIS 60

QY 61 RESGSGGRDYTFITSSLPEDIATYYCLQYDNLWTFGGTKVE 104

Db 61 RESGSGGRDYTFITSSLPEDIATYYCLQYDNLWTFGGTKLE 104

RESULT 2

S26329

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26329

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein ei
A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26329

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-104 <STA>

A:CROSS-references: EMBL:X59173; NID:G52309; PIDN:CAA41883.1; PID:gl334059

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 479; DB 2; Length 104;

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Best Local Similarity 84.6%; Pred. No. 9.8e-35;
Matches 88; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCSTQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60
Db 1 DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRLLIHYTSTLQPGIPS 60

Qy 61 RFGSGSGRDYFTTISLQPEDIATYCYLOYDNLWTFGGTKVE 104
Db 61 RFGSGSGRDYFTTISLQPEDIATYCYLOYDNLWTFGGTKLE 104

RESULT 3
C33936
Ig kappa chain V region (VH113) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C:Accession: C33936
A:Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A:Reference number: A33936; MUID:89282831; PMID:2471975
A:Accession: C33936
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <MEE>
A:Cross-references: GB:J04577; NID:9623187; PIDN:AAA60443.1; PID:9623189
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 478; DB 2; Length 106;
Best Local Similarity 83.0%; Pred. No. 1.2e-34;
Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCSTQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60
Db 1 DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRLLIHYTSTLQPGIPS 60

Qy 61 RFGSGSGRDYFTTISLQPEDIATYCYLOYDNLWTFGGTKVEIK 106
Db 61 RFGSGSGRDYFTTISLQPEDIATYCYLOYDNLWTFGGTKLEIK 106

RESULT 4
S09365
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S09365
R:Pedersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
A:Title: Direct evidence for intrastand DNA inversion of kappa immunoglobulin gene segm
A:Reference number: S09365; MUID:90098844; PMID:2513557
A:Accession: S09365
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-125 <FED>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 463.5; DB 2; Length 125;
Best Local Similarity 83.2%; Pred. No. 2.6e-33;
Matches 89; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVITTCSTQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60
Db 18 DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRLLIHYTSTLQPGIPS 77

Qy 61 RFGSGSGRDYFTTISLQPEDIATYCYLOYDNLWTFGGTKVEIK 106
Db 78 RFGSGSGRDYFTTISLQPEDIATYCYLOYDNLWTFGGTKLEIK 124
```

RESULT 5

```
PH1064
Ig light chain V region (clone 202.54) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1064
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B ce
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1064
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-97 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
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Query Match 80.4%; Score 452; DB 2; Length 97;
Best Local Similarity 85.6%; Pred. No. 2e-32;
Matches 83; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

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Qy 1 DIQMTQSPSSLSASVGRVITTCSTQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60
Db 1 DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRLLIHYTSTLQPGIPS 60

Qy 61 RFGSGSGRDYFTTISLQPEDIATYCYLOYDNLWTF 97
Db 61 RFGSGSGRDYFTTISLQPEDIATYCYLOYDNLWTF 97
```

RESULT 6

```
PL0270
Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0270
R:Shlomchik, M.; Mascellini, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic m
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0270
A:Molecule type: mRNA
A:Residues: 1-107 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-107/Region: framework 4
```

Query Match 79.4%; Score 446.5; DB 2; Length 107;
Best Local Similarity 79.4%; Pred. No. 6.5e-32;
Matches 85; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

```
Qy 1 DIQMTQSPSSLSASVGRVITTCSTQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60
Db 1 DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRLLIHYTSTLQPGIPS 60

Qy 61 RFGSGSGRDYFTTISLQPEDIATYCYLOYDNLWTFGGTKVEIK 106
Db 61 RFGSGSGRDYFTTISLQPEDIATYCYLOYDNLWTFGGTKLEIK 107
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RESULT 7

KIHURE

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

M protein - protein search, using sw model

un on: November 21, 2003, 15:20:03 ; Search time 10.5274 Seconds
(without alignments)
473.510 Million cell updates/sec

File: US-09-010-377-1

Perfect score: 562

Sequence: 1 DIQMTQSPSSLSASVGRVT.....YCLQYDNLMTFGQTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	443.5	78.9	108	1 KV10 HUMAN	P01607 homo sapien
2	439.5	78.2	108	1 KV1B HUMAN	P01594 homo sapien
3	421.5	75.0	108	1 KV1A HUMAN	P01605 homo sapien
4	419.5	74.6	108	1 KV1A HUMAN	P01593 homo sapien
5	419.5	74.6	108	1 KV1P HUMAN	P01608 homo sapien
6	419.5	74.6	108	1 KV1V HUMAN	P80362 homo sapien
7	413.5	73.6	108	1 KV1Q HUMAN	P01609 homo sapien
8	409.5	72.9	129	1 KV1Q HUMAN	P04431 homo sapien
9	409.5	72.8	107	1 KV1D HUMAN	P01596 homo sapien
10	408.5	72.7	108	1 KV1H HUMAN	P01610 homo sapien
11	402.5	71.6	108	1 KV1H HUMAN	P01600 homo sapien
12	397.5	70.7	108	1 KV1F HUMAN	P01598 homo sapien
13	396.5	70.6	108	1 KV1F HUMAN	P04430 homo sapien
14	390.5	69.5	108	1 KV1K HUMAN	P01603 homo sapien
15	388.5	69.1	108	1 KV1E HUMAN	P01597 homo sapien
16	386.5	68.8	108	1 KV1E HUMAN	P01604 homo sapien
17	385.5	68.6	108	1 KV1N HUMAN	P01606 homo sapien
18	384.5	68.4	108	1 KV1K HUMAN	P01595 homo sapien
19	383.5	68.2	108	1 KV1G HUMAN	P01599 homo sapien
20	381.5	68.2	129	1 KV1S HUMAN	P04432 homo sapien
21	381.5	67.9	108	1 KV1S HUMAN	P01611 homo sapien
22	376.5	67.0	134	1 KV4C HUMAN	P06314 homo sapien
23	371.5	66.1	108	1 KV5T MOUSE	P01643 mus musculu
24	368.5	65.5	117	1 KV1J HUMAN	P01602 homo sapien
25	366.5	65.2	128	1 KV5E MOUSE	P01637 mus musculu
26	365.5	64.9	133	1 KV4B HUMAN	P06313 homo sapien
27	364.5	64.9	108	1 KV5O MOUSE	P01648 mus musculu
28	363.5	64.7	108	1 KV5N MOUSE	P01647 mus musculu
29	362.5	64.4	109	1 KV1T HUMAN	P01612 homo sapien
30	362.5	64.4	117	1 KV1I HUMAN	P01601 homo sapien
31	361.5	64.3	108	1 KV5K MOUSE	P01644 mus musculu
32	359.5	64.0	108	1 KV5M MOUSE	P01646 mus musculu
33	358.5	63.8	108	1 KV5L MOUSE	P01645 mus musculu

34	356.5	63.4	112	1 KV1U HUMAN	P01613 homo sapien
35	348.5	62.0	114	1 KV4A HUMAN	P01625 homo sapien
36	348.5	61.9	129	1 KV3H HUMAN	P04207 homo sapien
37	346.5	61.6	129	1 KV3M HUMAN	P18136 homo sapien
38	345.5	61.5	108	1 KV5T MOUSE	P01653 mus musculu
39	345.5	61.4	115	1 KV5F MOUSE	P01638 mus musculu
40	341.5	60.8	108	1 KV5Q MOUSE	P01650 mus musculu
41	341.5	60.7	109	1 KV3E HUMAN	P01623 homo sapien
42	340.5	60.6	108	1 KV5S MOUSE	P01652 mus musculu
43	339.5	60.4	108	1 KV5U MOUSE	P04946 mus musculu
44	339.5	60.3	109	1 KV3D HUMAN	P01622 homo sapien
45	339.5	60.3	109	1 KV3F HUMAN	P01624 homo sapien

ALIGNMENTS

RESULT 1

ID	KV10 HUMAN	STANDARD;	PRT;	108 AA.
AC	P01607;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig kappa chain V-I region Rei.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RP	SEQUENCE.			
RX	MEDLINE=76023758; PubMed=809329;			
RA	Palm W., Hilschmann N.;			
RT	"The primary structure of a crystalline monoclonal immunoglobulin			
RT	kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation			
RT	and characterization of the tryptic peptides; the complete amino acid			
RT	sequence of the protein; a contribution to the elucidation of the			
RT	three-dimensional structure of antibodies, in particular their			
RT	combining site.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).			
[2]				
RN	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).			
RP	MEDLINE=76039968; PubMed=1182131;			
RX	Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;			
RA	"The molecular structure of a dimer composed of the variable portions			
RT	of the Bence-Jones protein Rei refined at 2.0-A resolution.";			
RL	Biochemistry 14:4943-4952(1975).			
CC	-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)			
CC	MARKER.			
CC	-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
DR	PIR; A91663; KIHURE.			
DR	PDB; 1REI; 17-FEB-84.			
DR	PDB; 1AR2; 12-NOV-97.			
DR	PDB; 1BWW; 29-DEC-99.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding activity; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003006; Ig MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS00835; IG_LIKE; 1.			
KW	Immunoglobulin V region; Bence-Jones protein; 3D-structure.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 34			
FT	COMPLEMENTARITY-DETERMINING-1.			
FT	DOMAIN 35 49			
FT	COMPLEMENTARITY-DETERMINING-2.			
FT	DOMAIN 50 56			
FT	COMPLEMENTARITY-DETERMINING-3.			
FT	DOMAIN 57 88			
FT	COMPLEMENTARITY-DETERMINING-3.			
FT	DOMAIN 89 97			
FT	DOMAIN 98 107			
FT	DISULFID 23 88			
FT	STRAND 4 7			

```

STRAND      10 13
TURN        15 16
STRAND      19 25
TURN        30 31
STRAND      33 38
TURN        40 41
STRAND      44 49
TURN        50 52
STRAND      53 54
TURN        56 57
TURN        60 61
STRAND      62 67
TURN        68 69
STRAND      70 75
HELIX       80 82
STRAND      85 90
TURN        97 98
STRAND     102 106
TURN       108 108
NON TER
SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match      78.9%; Score 443.5; DB 1; Length 108;
Best Local Similarity 81.1%; Pred. No. 4.9e-40; Indels 1; Gaps 1;
Matches 86; Conservative 9; Mismatches 10;

QY 1 DIQMTQSPSSLSASVGRVITITCKTSQDINKYMAWYQQTGPKAPRLLIHYTSALQFGIPS 60
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Db 1 DIQMTQSPSSLSASVGRVITITCKTSQDINKYMAWYQQTGPKAPRLLIHYTSALQAGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RFSGSGSRDYTTFTTSSLPQEDYATYCYQDNLNLTWFGQGTKEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGDYTTFTTSSLPQEDYATYCYQYQSLPYTFGQGTKEIK 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
KV1B HUMAN STANDARD; PRT; 108 AA.
ID ID KV1B HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehllhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146 (1975).
RN [2]
RP -I- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF THE KAPPA CHAIN REI.
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PDB; 1JTV5; 30-JAN-02.
DR PIR; A91653; K1HU4U.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.

```

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DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

Query Match      78.2%; Score 439.5; DB 1; Length 108;
Best Local Similarity 79.4%; Pred. No. 1.3e-39;
Matches 85; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITITCKTSQDINKYMAWYQQTGPKAPRLLIHYTSALQFGIPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVGRVITITCKTSQDINKYMAWYQQTGPKAPRLLIHYTSALQAGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RFSGSGSRDYTTFTTSSLPQEDYATYCYQDNLNLTWFGQGTKEIK 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGSGAHFTTFTTSSLPQEDYATYCYQYDYLEFTWFGQGTKEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
KV1M HUMAN STANDARD; PRT; 108 AA.
ID ID KV1M HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pcm) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684 (1976).
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
DR PIR; A01871; K1HULY.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

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GenCore version 5.1.6
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MM protein - protein search, using sw model

un on: November 21, 2003, 15:19:18 ; Search time 68.2397 Seconds
(without alignments)
286.100 Million cell updates/sec

File: US-09-010-377-2

Perfect score: 655

Sequence: 1 QVQLVQSGAEVKPKASVKV.....NYGVYMDYNGQGLTVTVSS 123

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	655	100.0	123	16 AAR81323	Humanized VLA-4 an
2	655	100.0	142	16 AAR81333	Human VLA-4 reshap
3	655	100.0	142	18 AAW2428	Humanised alpha-4
4	648	98.9	123	18 AAW2413	Humanised alpha-4
5	552	84.3	123	16 AAR81330	Mouse anti-VLA-4 a
6	544	83.1	140	16 AAR81327	Mouse VLA-4 antibo
7	544	83.1	140	18 AAW22410	Alpha-4 integrin m
8	523.5	79.9	120	19 AAW4124	Heavy chain variab
9	523.5	79.9	120	23 AAU79034	Humanised antibody

10	523.5	79.9	431	22 AAB30693	A fusion of single
11	523	79.8	136	16 AAR76681	Human/murine chime
12	523	79.8	136	17 AAW04396	Chimaeric human/mu
13	523	79.8	269	16 AAR76682	Human ONS-M21 anti
14	523	79.8	269	17 AAW04397	Chimaeric human/mu
15	515	78.6	119	16 AAR81325	Humanized VLA-4 an
16	515	78.6	119	18 AAW22426	Humanised alpha-4
17	512	78.2	119	16 AAR81324	Humanised VLA-4 an
18	512	78.2	119	18 AAW22425	Humanised alpha-4
19	507.5	77.5	135	21 AAB07969	A heavy chain vari
20	505.5	77.2	258	23 ABB05963	Monoclonal antibod
21	505.5	77.2	258	23 ABB05992	Mouse and human ch
22	505.5	77.2	258	23 ABB05996	Human monoclonal a
23	504.5	77.0	118	14 AAR37611	hIL2R Ab H chain v
24	503	76.8	119	20 AAY52717	Humanised ATR-5 H
25	503	76.8	119	22 AAB74978	Humanised ATR-5 H
26	501.5	76.6	258	23 ABB05991	Mouse and human ch
27	501.5	76.6	258	23 ABB05995	Human monoclonal a
28	499	76.2	119	20 AAY52719	Humanised ATR-5 H
29	499	76.2	119	22 AAB74980	Humanised ATR-5 H
30	496	75.7	136	17 AAR92084	Amino acid sequenc
31	496	75.7	136	23 ABB31443	Human 2*CL antibod
32	495	75.6	119	16 AAR81331	Humanised ATR-5 H
33	493	75.3	119	20 AAY52718	Humanised ATR-5 H
34	493	75.3	119	22 AAB74979	Humanised ATR-5 H
35	492	75.1	117	15 AAR57476	CDR-grafted anti-R
36	492	75.1	117	17 AAR92079	Marine 1308F VH CD
37	492	75.1	117	23 ABB31426	Humanised CDR-graf
38	492	75.1	136	15 AAR57481	Humanized 1308F VH
39	491.5	75.0	245	23 ABB45885	Human BlyS binding
40	491	75.0	119	20 AAY52708	Humanised ATR-5 H
41	491	75.0	119	22 AAB74959	Humanised ATR-5 H
42	489.5	74.7	120	18 AAW27551	Human Ab heavy cha
43	489	74.7	119	20 AAY52720	Humanised ATR-5 H
44	489	74.7	119	22 AAB74981	Humanised ATR-5 H
45	487.5	74.4	120	15 AAR74491	Humanised anti-CD1

ALIGNMENTS

RESULT 1

AAR81323

ID AAR81323 standard; Protein; 123 AA.

XX AAR81323;

XX AAR81323;

XX 02-APR-1996 (first entry)

XX Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.

XX Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;

XX antibody engineering.

XX Mus musculus.

XX WO9519790-A1.

XX 27-JUL-1995.

XX 25-JAN-1995; 95WO-US01219.

XX 25-JAN-1994; 94US-0186269.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

XX Bendig MM, Jones TS, Leger OJ, Saldanha J;

XX WPI; 1995-269276/35.

XX New humanised antibodies against VLA-4 - used for inhibiting

XX Alpha-4 integrin m

XX Heavy chain variab

XX inflammatory disease.

XX Claim 11; Page 69; 105pp; English.

XX The sequence encodes the mouse antibody 21.6 heavy chain variable

XX region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned

XX cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions

XX are linked to human constant regions in the construction of a humanized

XX antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are

XX modified using PCR primers (See AAQ99895-98) and then subcloned into

XX mammalian cell expression vectors containing human kappa or gamma-1

XX constant regions. In the humanized light chain, amino acids L45,

XX L49, L58 and L69 in the human kappa LC VR framework are replaced

XX by the amino acid present in the equivalent position of the mouse

XX 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are

XX transfected into COS cells. The humanized antibodies can be used

XX for inhibiting adhesion of a leukocyte to an endothelial cell and

XX for treating inflammatory diseases such as multiple sclerosis. They

XX can also be used in the treatment of stroke, cerebral traumas,

XX meningitis or encephalitis. The antibodies can also be used for

XX detecting VLA-4, for affinity purification or for generating

XX anti-idiotypic antibodies.

XX Sequence 123 AA;

XX Query Match 100.0%; Score 655; DB 16; Length 123;

XX Best Local Similarity 100.0%; Pred. No. 7.2e-53;

XX Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHVWRQAPGORLEWGMGRIDPANGYTKY 60

Db 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHVWRQAPGORLEWGMGRIDPANGYTKY 60

QY 61 DPKFQGRVITADTSASTAYMELSLRSEDVAVYVCAREGYGNYGVYAMDYWGQGLTVT 120

Db 61 DPKFQGRVITADTSASTAYMELSLRSEDVAVYVCAREGYGNYGVYAMDYWGQGLTVT 120

QY 121 VSS 123

Db 121 VSS 123

RESULT 2

AA81333

ID AA81333 standard; Protein; 142 AA.

XX AA81333;

XX 23-MAR-1996 (first entry)

XX Human VLA-4 reshaped antibody 21.6 light heavy variable region.

XX Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;

XX antibody engineering.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..19

XX /note= "signal peptide"

XX Region 20..49 "framework region 1"

XX /note= "framework region 1"

XX Region 50..54

XX /note= "complementarity determining region 1"

XX Region 55..68

XX /note= "framework region 2"

XX Region 69..85

XX /note= "complementarity determining region 2"

XX Region 86..117

XX /note= "framework region 3"

XX Region 118..131

XX /note= "complementarity determining region 3"

XX Region 132..142

XX /note= "framework region 4"

XX WO9519790-A1.

XX 27-JUL-1995.

XX 25-JAN-1995; 95WO-US01219.

XX 25-JAN-1994; 94US-0186269.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

XX Bendig MM, Jones TS, Leger OJ, Saldanha J;

XX WPI; 1995-269276/35.

XX N-PSDB; AAQ99894.

XX New humanised antibodies against VLA-4 - used for inhibiting

XX leukocyte adhesion to endothelial cells, partic. for treating

XX inflammatory disease.

XX Disclosure; Fig 11; 105pp; English.

XX The sequence represents the human reshaped antibody 21.6 heavy

XX chain variable region against leukocyte adhesion molecule VLA-4.

XX Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ99889)

XX regions are linked to human constant regions in the construction

XX of a humanized antibody against VLA-4. The 5' and 3' ends of the

XX mouse cDNAs are modified using PCR primers (AAQ99895-98) and then

XX subcloned into mammalian cell expression vectors containing human

XX kappa or gamma-1 constant regions. In the humanized heavy chain,

XX amino acids H27, H28, H29, H30, H44 and H71 in the human HC VR

XX framework are replaced by the amino acid present in the equivalent

XX position of the mouse 21.6 Ig H chain. Plasmids encoding the

XX chimeric antibodies are transfected into COS cells. The humanized

XX antibodies can be used to inhibit adhesion of a leukocyte to an

XX endothelial cell and to treat inflammatory diseases such as multiple

XX sclerosis. They can also be used in the treatment of stroke,

XX cerebral traumas, meningitis or encephalitis. The antibodies can

XX also be used for detecting VLA-4, for affinity purification or for

XX generating anti-idiotypic antibodies.

XX Sequence 142 AA;

XX Query Match 100.0%; Score 655; DB 16; Length 142;

XX Best Local Similarity 100.0%; Pred. No. 8.4e-53;

XX Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHVWRQAPGORLEWGMGRIDPANGYTKY 60

Db 20 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHVWRQAPGORLEWGMGRIDPANGYTKY 79

QY 61 DPKFQGRVITADTSASTAYMELSLRSEDVAVYVCAREGYGNYGVYAMDYWGQGLTVT 120

Db 80 DPKFQGRVITADTSASTAYMELSLRSEDVAVYVCAREGYGNYGVYAMDYWGQGLTVT 139

QY 121 VSS 123

Db 140 VSS 142

RESULT 3

AAW22428

ID AAW22428 standard; Protein; 142 AA.

XX AAW22428;

XX 09-DEC-1997 (first entry)

XX Humanised alpha-4 integrin antibody 21.6 VL version Ha.

XX Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;

XX asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;

XX metastasis; inflammatory bowel disease; rheumatoid arthritis;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

M protein - protein search, using sw model

un on: November 21, 2003, 15:21:54 ; Search time 23.1678 Seconds
(without alignments)
224.632 Million cell updates/sec

title: US-09-010-377-2
erfect score: 655
equence: 1 QVQLVQSGAEVKPKASVKY.....NYGVYANDYWGQGLTVVSS 123

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

earched: 328717 seqs, 42310858 residues

otal number of hits satisfying chosen parameters: 328717

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		Match	Length	DB ID	Description
	Score	%				
1	655	100.0	123	2	US-08-561-521-11	Sequence 11, Appl
2	655	100.0	123	5	PCT-US95-01219-11	Sequence 11, Appl
3	655	100.0	142	2	US-08-561-521-17	Sequence 17, Appl
4	655	100.0	142	5	PCT-US95-01219-17	Sequence 17, Appl
5	552	84.3	123	2	US-08-561-521-9	Sequence 9, Appl
6	552	84.3	123	5	PCT-US95-01219-9	Sequence 9, Appl
7	544	83.1	140	2	US-08-561-521-4	Sequence 4, Appl
8	544	83.1	140	5	PCT-US95-01219-4	Sequence 4, Appl
9	523	79.9	120	4	US-08-871-488A-19	Sequence 19, Appl
10	523	79.8	117	3	US-08-646-285A-132	Sequence 132, App
11	523	79.8	136	3	US-08-646-285A-99	Sequence 99, Appl
12	523	79.8	269	3	US-08-646-285A-109	Sequence 109, App
13	515	78.6	119	2	US-08-561-521-13	Sequence 13, Appl
14	515	78.6	119	5	PCT-US95-01219-13	Sequence 13, Appl
15	512	78.2	119	2	US-08-561-521-12	Sequence 12, Appl
16	512	78.2	119	5	PCT-US95-01219-12	Sequence 12, Appl
17	505	77.1	125	2	US-08-561-521-44	Sequence 44, Appl
18	505	77.1	125	5	PCT-US95-01219-44	Sequence 44, Appl
19	495	75.6	119	2	US-08-561-521-10	Sequence 10, Appl
20	495	75.6	119	5	PCT-US95-01219-10	Sequence 10, Appl
21	492	75.1	117	2	US-08-290-592E-17	Sequence 17, Appl
22	492	75.1	117	5	PCT-US95-10053-14	Sequence 14, Appl
23	492	75.1	117	5	PCT-US96-09448-17	Sequence 17, Appl
24	492	75.1	119	4	US-09-438-954-41	Sequence 41, Appl
25	491.5	75.0	118	2	US-08-232-081B-8	Sequence 8, Appl
26	489.5	74.7	120	4	US-09-025-769B-36	Sequence 36, Appl
27	489.5	74.7	120	4	US-09-025-769B-59	Sequence 59, Appl

28	486	74.2	140	3	US-08-836-561-63	Sequence 63, Appl
29	486	74.2	140	4	US-09-434-122-63	Sequence 63, Appl
30	484.5	74.0	135	1	US-08-137-117D-112	Sequence 112, App
31	484.5	74.0	135	2	US-08-436-717-112	Sequence 112, App
32	484.5	74.0	139	1	US-08-253-877C-19	Sequence 19, Appl
33	484.5	74.0	139	2	US-08-452-164A-19	Sequence 19, Appl
34	484.5	74.0	139	3	US-08-603-024-18	Sequence 14, Appl
35	484.5	74.0	139	4	US-08-450-809-14	Sequence 23, Appl
36	481	73.4	121	1	US-08-202-047-23	Sequence 23, Appl
37	481	73.4	121	3	US-08-964-690-23	Sequence 16, Appl
38	480.5	73.4	124	4	US-09-301-593-16	Sequence 41, Appl
39	480.5	73.4	124	4	US-09-301-593-41	Sequence 4, Appl
40	475	72.5	119	4	US-09-438-954-4	Sequence 74, Appl
41	474	72.4	140	3	US-08-836-561-74	Sequence 74, Appl
42	474	72.4	140	4	US-09-434-122-74	Sequence 53, Appl
43	473	72.2	123	1	US-08-482-882-53	Sequence 53, Appl
44	473	72.2	123	2	US-08-483-389-53	Sequence 53, Appl
45	473	72.2	123	2	US-08-487-113D-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-08-561-521-11
; Sequence 11, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-561-521-11

Query Match 100.0%; Score 655; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.7e-58;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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DM protein - protein search, using sw model

Run on: November 21, 2003, 15:27:54 ; Search time 45.9144 Seconds
(without alignments)
489.058 Million cell updates/sec

Title: US-09-010-377-2
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKPEASVKV.....NYGVYMDYWGQGLTVTVSS 123

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523.5	79.9	120	15	US-10-056-794-19
2	523.5	79.9	431	12	US-10-244-821-4
3	523.5	79.9	431	15	US-10-013-173-4
4	523.5	79.9	431	15	US-10-150-762-4
5	523.5	79.8	117	11	US-09-749-873-132
6	523.5	79.8	136	11	US-09-749-873-99
7	523.5	79.8	269	11	US-09-749-873-109
8	492.5	75.1	117	10	US-09-158-120A-17
9	492.5	75.1	119	15	US-10-233-996-41
10	491.5	75.0	245	11	US-09-880-748-1896
11	486	74.2	140	15	US-10-283-349-63
12	486	74.2	143	12	US-10-428-662-69
13	485.5	74.1	120	14	US-10-025-687-2
14	485.5	74.1	120	15	US-10-123-687-2
15	484	73.9	180	9	US-09-748-960-6

16	480.5	73.4	124	12	US-10-159-006-16	Sequence 16, Appl
17	480.5	73.4	124	12	US-10-159-006-41	Sequence 41, Appl
18	480.5	73.4	124	15	US-10-121-464-16	Sequence 16, Appl
19	479.5	73.2	252	11	US-09-880-748-1698	Sequence 1698, Ap
20	477	72.8	141	11	US-09-791-153A-60	Sequence 60, Appl
21	476.5	72.7	249	11	US-09-880-748-1290	Sequence 1290, Ap
22	476.5	72.7	249	11	US-09-880-748-1299	Sequence 1299, Ap
23	476.5	72.7	251	11	US-09-880-748-1146	Sequence 1146, Ap
24	475	72.5	119	15	US-10-233-996-4	Sequence 4, Appl
25	474.5	72.4	255	11	US-09-880-748-1156	Sequence 1156, Ap
26	474	72.4	140	15	US-10-283-349-74	Sequence 74, Appl
27	473	72.2	123	9	US-09-753-436-53	Sequence 53, Appl
28	473	72.2	123	12	US-10-163-942-53	Sequence 53, Appl
29	473	72.2	123	15	US-10-269-805-27	Sequence 27, Appl
30	472.5	72.1	124	12	US-10-159-006-12	Sequence 12, Appl
31	472.5	72.1	124	12	US-10-159-006-40	Sequence 40, Appl
32	472.5	72.1	124	15	US-10-121-464-12	Sequence 12, Appl
33	472	72.1	123	9	US-09-753-436-86	Sequence 86, Appl
34	472	72.1	123	12	US-10-163-942-86	Sequence 86, Appl
35	472	72.1	136	15	US-10-160-232-91	Sequence 91, Appl
36	470	71.8	136	11	US-09-749-873-29	Sequence 29, Appl
37	469.5	71.7	126	11	US-09-791-153A-61	Sequence 61, Appl
38	469.5	71.7	230	11	US-09-791-153A-53	Sequence 53, Appl
39	469	71.6	129	10	US-09-956-206A-77	Sequence 77, Appl
40	469	71.6	470	10	US-09-859-053-28	Sequence 28, Appl
41	468.5	71.5	124	12	US-10-159-006-14	Sequence 14, Appl
42	468.5	71.5	124	12	US-10-159-006-108	Sequence 108, App
43	468.5	71.5	124	15	US-10-121-464-14	Sequence 14, Appl
44	468.5	71.5	249	11	US-09-880-748-1730	Sequence 1730, Ap
45	468	71.5	248	11	US-09-880-748-1178	Sequence 1178, Ap

ALIGNMENTS

RESULT 1

US-10-056-794-19
; Sequence 19, Application US/10056794
; Publication No. US20030119078A1

GENERAL INFORMATION:

APPLICANT: Graves, Scott S.
Reno, John M.
Mallett, Robert W.
Hylarides, Mark D.
Searle, Stephen M.J.
Henry, Andrew H.
Pedersen, Jan T.
Rees, Anthony R.

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN PRETARGETING METHODS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/056,794

FILING DATE: 24-Jan-2002

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey Ph.D., Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 690022.527C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-056-794-19

Query Match 79.9%; Score 523.5; DB 15; Length 120;
Best Local Similarity 82.9%; Pred. No. 4.6e-43;
Matches 102; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLVQSGAEVKPGASVKVSKASGFNIKDTYIHWVRQAPGQRLWMGRIDPANGYTKY 60
Db 1 QVQLVQSGAEVKPGASVKVSKASGFNIKDTYIHWVRQAPGQGLQWMGRIDPANGTKC 60

QY 61 DPKEQGRVTITADTSASTAYMELSSLRSEDTAVVYCARGGYGVYAMDYWGQGLT 120
Db 61 DLSFGQGRVTITADTSINTAYMELSSLRSDDTAVVYCSREVL---TGTWSLDYWGQGLT 117

QY 121 VSS 123
Db 118 VSS 120

RESULT 2
US-10-244-821-4
; Sequence 4, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence for huNR-LU-10
; OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
US-10-244-821-4

Query Match 79.9%; Score 523.5; DB 12; Length 431;
Best Local Similarity 82.9%; Pred. No. 1.9e-42;
Matches 102; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLVQSGAEVKPGASVKVSKASGFNIKDTYIHWVRQAPGQRLWMGRIDPANGYTKY 60
Db 148 QVQLVQSGAEVKPGASVKVSKASGFNIKDTYIHWVRQAPGQGLQWMGRIDPANGTKS 207

QY 61 DPKEQGRVTITADTSASTAYMELSSLRSEDTAVVYCARGGYGVYAMDYWGQGLT 120
Db 208 DLSFGQGRVTITADTSINTAYMELSSLRSDDTAVVYCSREVL---TGTWSLDYWGQGLT 264

QY 121 VSS 123
Db 265 VSS 267

RESULT 3
US-10-013-173-4
; Sequence 4, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence for huNR-LU-10
; OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
US-10-013-173-4

Query Match 79.9%; Score 523.5; DB 15; Length 431;
Best Local Similarity 82.9%; Pred. No. 1.9e-42;
Matches 102; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLVQSGAEVKPGASVKVSKASGFNIKDTYIHWVRQAPGQRLWMGRIDPANGYTKY 60
Db 148 QVQLVQSGAEVKPGASVKVSKASGFNIKDTYIHWVRQAPGQGLQWMGRIDPANGTKS 207

QY 61 DPKEQGRVTITADTSASTAYMELSSLRSEDTAVVYCARGGYGVYAMDYWGQGLT 120
Db 208 DLSFGQGRVTITADTSINTAYMELSSLRSDDTAVVYCSREVL---TGTWSLDYWGQGLT 264

QY 121 VSS 123
Db 265 VSS 267

RESULT 4
US-10-150-762-4
; Sequence 4, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150,762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence for huNR-LU-10
; OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
US-10-150-762-4

Query Match 79.9%; Score 523.5; DB 15; Length 431;

GenCore version 5.1.6
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CDM protein - protein search, using sw model

Run on: November 21, 2003, 15:20:03 ; Search time 12.2158 Seconds
(without alignments)
473.510 Million cell updates/sec

Title: US-09-010-377-2

Perfect score: 655

Sequence: 1 QVQLVQSGAEVKPGASVKV.....NYGVAMDYWGQGLTVTVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	427.5	65.3	147	1 HV1C_HUMAN	P01744 homo sapien
2	409	62.4	120	1 HV03_MOUSE	P01747 mus musculus
3	408.5	62.4	139	1 HV07_MOUSE	P01751 mus musculus
4	405	61.8	117	1 HV1B_HUMAN	P01743 homo sapien
5	399	60.9	140	1 HV02_MOUSE	P01746 mus musculus
6	396	60.5	117	1 HV1G_HUMAN	P23083 homo sapien
7	390	59.5	117	1 HV1A_HUMAN	P01742 homo sapien
8	378	57.7	117	1 HV13_MOUSE	P01757 mus musculus
9	375.5	57.3	118	1 HV51_MOUSE	P06330 mus musculus
10	373	56.9	117	1 HV12_MOUSE	P01756 mus musculus
11	371.5	56.7	137	1 HV11_MOUSE	P01755 mus musculus
12	369	56.3	138	1 HV48_MOUSE	P03980 mus musculus
13	364.5	55.6	120	1 HV50_MOUSE	P06329 mus musculus
14	360	55.0	121	1 HV01_MOUSE	P01745 mus musculus
15	360	55.0	136	1 HV15_MOUSE	P01759 mus musculus
16	355	54.2	125	1 HV1F_HUMAN	P06326 homo sapien
17	349.5	53.4	120	1 HV1H_HUMAN	P80421 homo sapien
18	349	53.3	117	1 HV09_MOUSE	P01753 mus musculus
19	344.5	52.6	114	1 HV00_MOUSE	P01741 mus musculus
20	338	51.6	117	1 HV04_MOUSE	P01748 mus musculus
21	336	51.3	117	1 HV06_MOUSE	P01750 mus musculus
22	333.5	50.9	136	1 HV16_MOUSE	P01783 mus musculus
23	333	50.8	117	1 HV10_MOUSE	P01754 mus musculus
24	330.5	50.5	124	1 HV1E_HUMAN	P01761 homo sapien
25	329	50.2	117	1 HV14_MOUSE	P01758 mus musculus
26	329	50.2	117	1 HV49_MOUSE	P06328 mus musculus
27	326	49.8	117	1 HV52_MOUSE	P06327 mus musculus
28	326	49.8	123	1 HV24_MOUSE	P01793 mus musculus
29	325.5	49.7	119	1 HV17_MOUSE	P01807 mus musculus
30	325.5	49.7	124	1 HV1D_HUMAN	P01760 homo sapien
31	324.5	49.5	119	1 HV38_MOUSE	P01808 mus musculus
32	323.5	49.4	119	1 HV40_MOUSE	P01810 mus musculus
33	320.5	48.9	122	1 HV3G_HUMAN	P01768 homo sapien

34	319	48.7	117	1 HV42_MOUSE	P01812 mus musculus
35	318.5	48.6	122	1 HV3A_HUMAN	P01762 homo sapien
36	318	48.5	121	1 HV3J_HUMAN	P01771 homo sapien
37	317	48.4	123	1 HV19_MOUSE	P01788 mus musculus
38	315	48.1	123	1 HV18_MOUSE	P01787 mus musculus
39	314.5	48.0	122	1 HV21_MOUSE	P01790 mus musculus
40	314	47.9	117	1 HV05_MOUSE	P01749 mus musculus
41	313	47.8	123	1 HV25_MOUSE	P01794 mus musculus
42	313	47.8	142	1 HV01_RAT	P01805 rattus norv
43	312	47.6	118	1 HV39_MOUSE	P01809 mus musculus
44	312	47.6	123	1 HV22_MOUSE	P01791 mus musculus
45	311.5	47.6	122	1 HV3H_HUMAN	P01769 homo sapien

ALIGNMENTS

RESULT 1
HV1C_HUMAN
ID HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor [Fragments].
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Moigaard H.V., Houghton M., Derbyshire R.B., Viney J., Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978).
CC -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; 1MCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT DOMAIN 20 131 IG-LIKE.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match. 65.3%; Score 427.5; DB 1; Length 147;

Best Local Similarity 64.1%; Pred No. 1.1e-36;

Matches 82; Conservative 16; Mismatches 25; Indels 5; Gaps 1;

```

QY 1 QVQLVQSGAEVKKPGASVKVSKASGPNFKDTYIHVWRQAPGQRLWGMGRIDPANGYTKY 60
DB 20 QQLVQSGAEVKKPGASVRSKASGYTFIDSYIHWRQAPGHLWGVGNPNFGQNTY 79
QY 61 DKPQGRVTITADTSASTAYMELSLRSSEDTAVYYCAR-----EGYNGYGVYANDYWGQ 115
DB 80 APRFQGRVTMTDASFTAYMQLSLRSLSRSDSAVFYCAKSDPFWSDYFNFDYSYTLDDWGQ 139
QY 116 GLTVTVSS 123
DB 140 GTTVTVSS 147

RESULT 2
HV03 MOUSE
ID HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse)
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=83131846; PubMed=6186498;
SIEKEVITZ M., Geffer M.L., Brodeur P., Riblet R.,
MARSHAK-ROTHSTEIN A.;
"the genetic basis of antibody production: the dominant anti-arsenate
idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP: P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120
FT SEQUENCE 120 AA; 13307 MW; PF0424A167B654AF CRC64;

Query Match 62.4%; Score 409; DB 1; Length 120;
Best Local Similarity 63.1%; Pred. No. 6.5e-35;
Matches 77; Conservative 18; Mismatches 25; Indels 2; Gaps 1;

QY 2 QVQLVQSGAEVKKPGASVKVSKASGPNFKDTYIHVWRQAPGQRLWGMGRIDPANGYTKYD 61
DB 1 VQLQQSGAEVLVRAGSSVKMSCKASGYTFISYGINWVQKRPQCGLEMTGYNPGNGYTKYN 60
QY 62 PKFQGRVTITADTSASTAYMELSLRSSEDTAVYYCAREGYNGYGVYANDYWGQGLTVTV 121
DB 61 EKFKGKTLTVDKSSSTAYMQLSLRSLSRSDSAVFYCARSVYIG--GSYTFDYWGQGLTLTV 118
QY 122 SS 123
DB 119 SS 120

RESULT 3
HV07 MOUSE
ID HV07 MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; J00529; AAA38170.1; -.
DR PIR; A90809; MHMS18.
DR PDB; 1AGU; 27-MAY-98.
DR PDB; 1ASW; 15-JUL-98.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
FT SEQUENCE 139 AA; 15419 MW; 1BS7DD4FD0C9F465 CRC64;

Query Match 62.4%; Score 408.5; DB 1; Length 139;
Best Local Similarity 62.6%; Pred. No. 8.6e-35;
Matches 77; Conservative 18; Mismatches 25; Indels 3; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGPNFKDTYIHVWRQAPGQRLWGMGRIDPANGYTKY 60
DB 20 QVQLQSGAEVLVRAGSSVKMSCKASGYTFISYGINWVQKRPQCGLEMTGYNPGNGYTKY 79
QY 61 DKPQGRVTITADTSASTAYMELSLRSSEDTAVYYCAREGYNGYGVYANDYWGQGLTVTV 120
DB 80 NEKFKKTLTVDKPSSTAYMQLSLRSLSRSDSAVFYCARVDYIGS---SYFDYWGQGLTLTV 136
QY 121 VSS 123
DB 137 VSS 139

RESULT 4
HV1B HUMAN
ID HV1B HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	457.5	69.8	124	4	Q9UL92	Q9UL92 homo sapien
2	440.5	67.3	159	4	Q96QSO	Q96QSO homo sapien
3	440	67.2	468	11	Q9JL31	Q9JL31 mus musculus
4	432	66.0	109	11	Q9JL85	Q9JL85 mus musculus
5	432	66.0	119	4	Q9UL94	Q9UL94 homo sapien
6	432	66.0	614	4	Q96GA6	Q96GA6 homo sapien
7	428	65.3	119	5	Q9GY22	Q9GY22 schistosoma
8	428	65.3	125	4	Q9UL95	Q9UL95 homo sapien
9	427	65.2	146	11	Q924Q3	Q924Q3 mus musculus
10	432	64.4	473	11	Q9D8L4	Q9D8L4 mus musculus
11	415.5	63.4	145	11	Q924R1	Q924r1 mus musculus
12	415.5	63.4	145	11	Q924R1	Q924r1 mus musculus
13	414.5	63.3	482	11	Q8K172	Q8K172 mus musculus
14	412	62.9	146	11	Q924R8	Q924r8 mus musculus
15	411.5	62.8	116	4	Q9UL89	Q9UL89 homo sapien
16	409.5	62.5	145	11	Q924Q6	Q924q6 mus musculus

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Db 1 EVOLVESGAEVKKPGASVKVSKASGYTFSSYHWHVWVQAPGQGLEWMGINPSGGSTSY 60
Qy 61 DPKFGQGVTTTADTSASTAYMELSSLSRSEDVAVYVCAREGYGNYGVYAM-----DY 112
Db 61 AQKFGQGVTTTADTSASTAYMELSSLSRSEDVAVYVCAR-----GLYVVVPAAFSEFDY 113
Qy 113 WQGGTLTVVSS 123
Db 114 WQGGTLTVVSS 124

RESULT 2
Q96QSO PRELIMINARY; PRT; 159 AA.
ID Q96QSO;
AC Q96QSO;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D295337B881FAF02 CRC64;

Query Match 67.3%; Score 440.5; DB 4; Length 159;
Best Local Similarity 64.9%; Pred. No. 6.4e-39;
Matches 87; Conservative 13; Mismatches 19; Indels 15; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGFIKDTYIHVWVQAPGQGLEWMGRIDPANGYTKY 60
Db 20 QVQLVQSGAEVKKPGASVKVSKASGYTFSSYHWHVWVQAPGQGPPEWGMVGNPSGGARY 79
Qy 61 DPKFGQGVTTTADTSASTAYMELSSLSRSEDVAVYVCARE-----GYGNYGVYA 109
Db 80 SQKFGQGVTTTADTSASTAYMELSSLSRSEDVAVYFCAREMEITFGGAVSKGFY----YYG 135

Qy 110 MDYWGQGLTVVSS 123
Db 136 MDVWGQGLTVVSS 149

RESULT 3
Q99L31 PRELIMINARY; PRT; 468 AA.
ID Q99L31;
AC Q99L31;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSP; F01842; 7FAB.
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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 67.2%; Score 440; DB 11; Length 468;
Best Local Similarity 67.5%; Pred. No. 2.8e-38;
Matches 83; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGFIKDTYIHVWVQAPGQGLEWMGRIDPANGYTKY 60
Db 20 EVQLQSGAEVLRPGASVKLSCTASGFIKDSLHWHVKQRPQGLEWIGWIDPEDGETKY 79
Qy 61 DPKFGQGVTTTADTSASTAYMELSSLSRSEDVAVYVCAREGYGNYGVYAMDYWGQGLTVT 120
Db 80 APKFDKATITADTSSTNTAYLQLSSLTSEDVAVYCARNLVGGY----YDYWGQGLTIT 135
Qy 121 VSS 123
Db 136 VSS 138

RESULT 4
Q9JL85 PRELIMINARY; PRT; 109 AA.
ID Q9JL85;
AC Q9JL85;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DB (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/C;
RA MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206021; AAP69319.1; -.
DR HSP; F01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 66.0%; Score 432; DB 11; Length 109;
Best Local Similarity 68.7%; Pred. No. 3.2e-38;
Matches 79; Conservative 15; Mismatches 15; Indels 6; Gaps 1;

Qy 9 AEVKKPGASVKVSKASGFIKDTYIHVWVQAPGQGLEWMGRIDPANGYTKYDPKFGQGV 68
Db 1 AELVKPGASVKLSCTASGFIKDTYIHVWVQRPQGLEWIGRIDPATGSHKYPKFGKA 60
Qy 69 TITADTSASTAYMELSSLSRSEDVAVYVCAREGYGNYGVYAMDYWGQGLTVVSS 123
Db 61 TITSDTSNTAYLQLSSLTSEDVAVYCVRR-----GAVVFDYWGQGLTALTVSS 109
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M protein - protein search, using sw model

un on: November 21, 2003, 15:21:54 , Search time 2.82534 Seconds
(without alignments)
224.632 Million cell updates/sec

itle: US-09-010-377-3

erfect score: 15
equence: 1 XXXXXXXXXXXXX 15

oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

earched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCUTS.COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match		DB ID	Description
		Match	Length		
1	0	0.0	1	1	US-07-820-154A-12
2	0	0.0	1	1	US-07-791-213D-24
3	0	0.0	1	1	US-07-791-213D-40
4	0	0.0	1	1	US-08-174-365A-57
5	0	0.0	1	1	US-07-789-913-23
6	0	0.0	1	1	US-07-789-913-25
7	0	0.0	1	1	US-08-049-794-23
8	0	0.0	1	1	US-08-049-794-25
9	0	0.0	1	1	US-08-433-037-12
10	0	0.0	1	1	US-08-448-606-4
11	0	0.0	1	1	US-07-869-933-16
12	0	0.0	1	1	US-08-293-150A-24
13	0	0.0	1	1	US-08-293-150A-40
14	0	0.0	1	1	US-08-496-847-23
15	0	0.0	1	1	US-08-496-847-25
16	0	0.0	1	2	US-08-742-774-23
17	0	0.0	1	2	US-08-742-774-25
18	0	0.0	1	2	US-08-675-354-23
19	0	0.0	1	2	US-08-675-354-25
20	0	0.0	1	2	US-08-097-554A-12
21	0	0.0	1	2	US-08-965-918-23
22	0	0.0	1	2	US-08-965-918-25
23	0	0.0	1	2	US-09-138-439-23
24	0	0.0	1	2	US-09-138-439-25
25	0	0.0	1	3	US-08-480-640A-12
26	0	0.0	1	3	US-08-613-400A-23
27	0	0.0	1	3	US-08-613-400A-25

28	0	0.0	1	3	US-08-801-092-10	Sequence 10, Appl
29	0	0.0	1	3	US-08-801-092-17	Sequence 17, Appl
30	0	0.0	1	3	US-08-801-092-24	Sequence 24, Appl
31	0	0.0	1	3	US-08-801-092-31	Sequence 31, Appl
32	0	0.0	1	3	US-08-801-092-38	Sequence 38, Appl
33	0	0.0	1	3	US-08-801-092-45	Sequence 45, Appl
34	0	0.0	1	3	US-09-298-017-23	Sequence 23, Appl
35	0	0.0	1	3	US-09-298-017-25	Sequence 25, Appl
36	0	0.0	1	3	US-08-295-802-12	Sequence 12, Appl
37	0	0.0	1	3	US-09-332-379A-23	Sequence 23, Appl
38	0	0.0	1	3	US-09-392-979A-25	Sequence 25, Appl
39	0	0.0	1	3	US-09-103-663-16	Sequence 16, Appl
40	0	0.0	1	3	US-08-488-237A-12	Sequence 12, Appl
41	0	0.0	1	3	US-09-117-927-5	Sequence 5, Appli
42	0	0.0	1	4	US-08-375-992A-12	Sequence 12, Appl
43	0	0.0	1	4	US-09-315-113-10	Sequence 10, Appl
44	0	0.0	1	4	US-09-315-113-17	Sequence 17, Appl
45	0	0.0	1	4	US-09-315-113-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-07-820-154A-12
; Sequence 12, Application US/07820154A
; Patent No. 5382425
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; APPLICANT: Junker M.S., David E
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07820.154A
; FILING DATE: 19920113
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-820-154A-12

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 V 1

RESULT 2

US-07-791-213D-24

/ Sequence 24, Application US/07791213D
/ Patent No. 5409895
/ GENERAL INFORMATION:
/ APPLICANT: MORISHITA, Hideaki
/ APPLICANT: KANAMORI, Toshinori
/ APPLICANT: NOBUHARA, Masahiro
/ TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
/ TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
/ TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
/ TITLE OF INVENTION: TREATING USING THE SAME
/ NUMBER OF SEQUENCES: 108
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: P.O. Box 1404
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22313-1404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07791,213D
/ FILING DATE: 13-NOV-1991
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 2-306745
/ FILING DATE: 13-NOV-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meuth, Donna M
/ REGISTRATION NUMBER: 36,607
/ REFERENCE/DOCKET NUMBER: 029650-032
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-07-791-213D-24

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 C 1

RESULT 3
US-07-791-213D-40
/ Sequence 40, Application US/07791213D
/ Patent No. 5409895
/ GENERAL INFORMATION:
/ APPLICANT: MORISHITA, Hideaki
/ APPLICANT: KANAMORI, Toshinori
/ APPLICANT: NOBUHARA, Masahiro
/ TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
/ TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
/ TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
/ TITLE OF INVENTION: TREATING USING THE SAME
/ NUMBER OF SEQUENCES: 108
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: P.O. Box 1404
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States

/ ZIP: 22313-1404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07791,213D
/ FILING DATE: 13-NOV-1991
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 2-306745
/ FILING DATE: 13-NOV-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meuth, Donna M
/ REGISTRATION NUMBER: 36,607
/ REFERENCE/DOCKET NUMBER: 029650-032
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-07-791-213D-40

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 C 1

RESULT 4
US-08-174-365A-57
/ Sequence 57, Application US/08174365A
/ Patent No. 5478809
/ GENERAL INFORMATION:
/ APPLICANT: Seiichi TANIDA et al
/ TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
/ NUMBER OF SEQUENCES: 106
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wenderoth, Lind & Ponack
/ STREET: 805 Fifteenth Street, N.W., #700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: Wordperfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/174,365A
/ FILING DATE: December 28, 1993
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warren M. Cheek, Jr.
/ REGISTRATION NUMBER: 33,367
/ REFERENCE/DOCKET NUMBER:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-8850
/ TELEFAX:
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 57:

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DOM protein - protein search, using sw model

Run on: November 21, 2003, 15:21:14 ; Search time 2.77397 Seconds
(without alignments)
520.023 Million cell updates/sec

Title: US-09-010-377-3

Perfect score: 15

Sequence: 1 XXXXXXXXXXXXX 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %	Score	Match	Length	ID	Description
1	0	0.0	0	3	3	RHDTTO
2	0	0.0	0	3	3	RHPGT
3	0	0.0	0	3	3	RHSHT
4	0	0.0	0	3	3	A92971
5	0	0.0	0	3	3	GKHU
6	0	0.0	0	3	3	A60898
7	0	0.0	0	3	3	A23751
8	0	0.0	0	3	3	B23751
9	0	0.0	0	3	3	A33802
10	0	0.0	0	3	3	A22565
11	0	0.0	0	3	3	PQ0010
12	0	0.0	0	3	3	S13894
13	0	0.0	0	3	3	A43391
14	0	0.0	0	3	3	E37196
15	0	0.0	0	3	3	F37196
16	0	0.0	0	3	3	I50412
17	0	0.0	0	3	3	PT0636
18	0	0.0	0	3	3	PT0578
19	0	0.0	0	3	3	PT0571
20	0	0.0	0	3	3	PT0622
21	0	0.0	0	3	3	I78890
22	0	0.0	0	3	3	S68328
23	0	0.0	0	3	3	TL13892
24	0	0.0	0	4	1	ECXAA
25	0	0.0	0	4	2	S18401
26	0	0.0	0	4	2	A02147
27	0	0.0	0	4	2	A32039
28	0	0.0	0	4	2	ECNK
29	0	0.0	0	4	2	PL0140

30 0 0.0 4 2 PL0146 carbon-monoxide de
31 0 0.0 4 2 A37832 phenol 2-monooxyge
32 0 0.0 4 2 A48360 gamma subunit of p
33 0 0.0 4 2 I40697 biotin A - Citroba
34 0 0.0 4 2 A61300 22K superhelical D
35 0 0.0 4 2 I57745 D-mannonate hydrol
36 0 0.0 4 2 A41890 protein D - Escher
37 0 0.0 4 2 S43014 hypothetical prote
38 0 0.0 4 2 D41654 hypothetical prote
39 0 0.0 4 2 B43848 cell surface adhes
40 0 0.0 4 2 I40505 hypothetical prote
41 0 0.0 4 2 I40870 phospholipase C (E
42 0 0.0 4 2 I40804 endoglucanase F -
43 0 0.0 4 2 T46627 hypothetical prote
44 0 0.0 4 2 S53508 starvation-induced
45 0 0.0 4 2 S17255 ribosomal protein

ALIGNMENTS

RESULT 1

RHDTTO

thyroliberin - Bombina orientalis

C:Species: Bombina orientalis

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: A90919; A01415

R:Yasuhara, T.; Nakajima, T.

Chem. Pharm. Bull. 23, 3301-3303, 1975

A:Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.

A:Reference number: A90919; MUID:76138399; PMID:815011

A:Accession: A90919

A:Molecule type: protein

A:Residues: 1-3 <YAS>

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 Q 1

RESULT 2

RHPGT

thyroliberin - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: A01415

R:Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.

Biochemistry 9, 1103-1106, 1970

A:Title: Structure of porcine thyrotropin releasing hormone.

A:Reference number: A90560; MUID:70136150; PMID:4984938

A:Accession: A01415

A:Molecule type: protein

A:Residues: 1-3 <NAI>

R:Boiler, J.; Enzmann, F.; Folkers, K.; Bowers, C.V.; Schally, A.V.

Biochem. Biophys. Res. Commun. 37, 705-710, 1969

A:Title: The identity of chemical and hormonal properties of the thyrotropin releasing hc

A:Reference number: A90167; MUID:70039904; PMID:4982117

A:Contents: annotation

A>Note: biological activities and Rf values (in 17 chromatographic systems) of the synthe

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 Q 1

RESULT 3
RHSHT
thyroliberin - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A93750; A01415
R; Desiderio Jr., D.M.; Burgess, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
Org. Mass Spectrom. 5; 221-228, 1971
A/Title: The elucidation of the primary structure of the hypothalamic thyroid stimulating hormone
A/Reference number: A93750
A/Accession: A93750
A/Molecule type: protein
A/Residues: 1-3 <DES>
R; Burgess, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.
Nature 226, 321-325, 1970
A/Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.
A/Reference number: A93161; MUID:70163386; PMID:4985794
A/Contents: annotation
A/Note: physicochemical characteristics and biological activities of the natural and synthetic thyroliberin precursor
C/Superfamily: thyroliberin precursor
C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 Q 1

RESULT 4
A92971
thyroliberin - eastern newt (tentative sequence)
C/Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A92971; A01415
R; Grimm-Jorgensen, Y.; McKelvy, J.F.
J. Neurochem. 23, 471-478, 1974
A/Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain
A/Reference number: A92971; MUID:75035605; PMID:4214528
A/Accession: A92971
A/Molecule type: protein
A/Residues: 1-3 <GRI>
A/Note: a peptide with the chromatographic and electrophoretic characteristics of thyroliberin, or glutamic acid
C/Superfamily: thyroliberin precursor
C/Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 Q 1

RESULT 5
GXHU
growth-modulating peptide - human

C/Species: Homo sapiens (man)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A01421
R; Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A/Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A/Reference number: A01421; MUID:77162369; PMID:858356
A/Accession: A01421
A/Molecule type: protein
A/Residues: 1-3 <SCH>
A/Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit growth of others
C/Superfamily: unassigned animal peptides

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 G 1

RESULT 6
A60898
bursin - chicken
C/Species: Gallus gallus (chicken)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A60898
R; Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 231, 997-999, 1986
A/Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of the bursa of Fabricius
A/Reference number: A60898; MUID:86122916; PMID:3484838
A/Accession: A60898
A/Molecule type: protein
A/Residues: 1-3 <AUD>
C/Superfamily: unassigned animal peptides
C/Keywords: amidated carboxyl end; hormone
F;3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 K 1

RESULT 7
A23751
spinal cord peptide SCP-4 - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A23751
R; Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985
A/Reference number: A23751; MUID:85250425; PMID:4015098
A/Accession: A23751
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-3 <HSI>
C/Superfamily: unassigned animal peptides

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 Q 1

RESULT 8

GenCore version 5.1.6
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DOM protein - protein search, using sw model

Run on: November 21, 2003, 15:20:03 ; Search time 1.48973 Seconds
(without alignments)
473.510 Million cell updates/sec

Title: US-09-010-377-3

Perfect score: 15

Sequence: 1 XXXXXXXXXXXXXXX 15

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	0.0	3	1 GRWM_HUMAN	P01157 homo sapien
2	0	0.0	3	1 LUXE_VIBFI	P24272 vibrio fisc
3	0	0.0	3	1 THYL_PIG	P01151 sus scrofa
4	0	0.0	4	1 ACHI_ACHFU	P35904 achatina fu
5	0	0.0	4	1 DCML_PSECH	P19916 pseudomonas
6	0	0.0	4	1 DCMS_PSECH	P19918 pseudomonas
7	0	0.0	4	1 EOSI_HUMAN	P02731 homo sapien
8	0	0.0	4	1 FAR3_HIRME	P43562 hirudo medi
9	0	0.0	4	1 FAR4_HIRME	P43563 hirudo medi
10	0	0.0	4	1 FFKA_ANTEL	P58705 anthopleura
11	0	0.0	4	1 FLRF_HIRME	P42561 hirudo medi
12	0	0.0	4	1 FLRN_ANTEL	P58707 anthopleura
13	0	0.0	4	1 FMRF_MACNI	P01162 macrocallis
14	0	0.0	4	1 FVEI_ANTEL	P58706 anthopleura
15	0	0.0	4	1 OC31_OCTMI	P58648 octopus min
16	0	0.0	4	1 OC33_OCTMI	P58649 octopus min
17	0	0.0	4	1 RM01_YEAST	P36515 saccharomyc
18	0	0.0	4	1 TUFT_HUMAN	P01858 homo sapien
19	0	0.0	5	1 ALI4_CARMA	P81817 carcinus ma
20	0	0.0	5	1 B10A_CITFR	P13071 citrobacter
21	0	0.0	5	1 B10B_CITFR	P12997 citrobacter
22	0	0.0	5	1 BP7F_BOTIN	P30425 bothrops in
23	0	0.0	5	1 EI03_LITRU	P82099 litoria rub
24	0	0.0	5	1 EI04_LITRU	P82100 litoria rub
25	0	0.0	5	1 FARP_ARTTR	P41853 artiopesthi
26	0	0.0	5	1 FARP2_PARMA	P81864 pardachirus
27	0	0.0	5	1 PRCT_PERAM	P01373 periplaneta
28	0	0.0	5	1 PSK_DAUCA	P58261 daucus caro
29	0	0.0	5	1 RE31_LITRU	P82070 litoria rub
30	0	0.0	5	1 RE21_LITRU	P82071 litoria rub
31	0	0.0	5	1 RE31_LITRU	P82072 litoria rub
32	0	0.0	5	1 RE32_LITRU	P82073 litoria rub
33	0	0.0	5	1 SUGA_ACHDO	P19991 acheta dome

34 0 0.0 5 1 TPIS_CANFA P54714 canis famli
35 0 0.0 5 1 TEM3_ECOLI P13973 escherichia
36 0 0.0 5 1 UC22_MAIZE P06628 zea mays (m
37 0 0.0 5 1 UF01_MOUSE P38639 mus musculu
38 0 0.0 5 1 UXA4_CHLTR P38005 chlamydia t
39 0 0.0 6 1 ACPH_RABIT P25154 oryctolagus
40 0 0.0 6 1 ASP2_LACSN P82655 lactobacill
41 0 0.0 6 1 C1P1_MYTED P13736 mytilus edu
42 0 0.0 6 1 C1P2_MYTED P13737 mytilus edu
43 0 0.0 6 1 EI01_LITRU P82096 litoria rub
44 0 0.0 6 1 FARP_MONEX P41966 moniezia ex
45 0 0.0 6 1 LOK1_LOCM1 P41491 locusta mig

ALIGNMENTS

RESULT 1
GRWM_HUMAN STANDARD; PRT; 3 AA.
ID P01157;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
CC -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
CC GO: GO:0001558; P:regulation of cell growth; NAS.
DR GO: GO:0001558; P:regulation of cell growth; NAS.
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 G 1
RESULT 2
LUXE_VIBFI STANDARD; PRT; 3 AA.
ID P24272;
AC 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE protein synthetase) (Fragment).
LN LUXE.
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072226; PubMed=2254256;
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT site for the lux operon.";
RL J. Bacteriol. 172:6797-6802(1990).
CC -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS

CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
 CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
 CC an acyl-protein thioester.
 CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M62812; -; NOT ANNOTATED_CDS.
 CC KW Luminescence; Ligase.
 CC FT NON TER 1 1
 CC SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;
 CC
 CC Query Match 0.0%; Score 0; DB 1; Length 3;
 CC Best Local Similarity 0.0%; Pred. No. 0;
 CC Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 1 X 1
 CC Db 1 I 1
 CC
 CC RESULT 3
 CC THYL_PIG STANDARD; PRT; 3 AA.
 CC ID THYL_PIG
 CC AC P01151;
 CC DT 21-JUL-1986 (Rel. 01, Created)
 CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
 CC OS Sus scrofa (pig);
 CC OS Ovis aries (Sheep);
 CC OS Bombina orientalis (Oriental fire-bellied toad), and
 CC OS Notoththalmus viridescens (Eastern newt) (Triturus viridescens).
 CC OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CC OX NCBI_TaxID=9823, 9940, 8346, 8316;
 CC [1]
 CC SEQUENCE.
 CC SPECIES=Pig; TISSUE=Hypothalamus;
 CC MEDLINE=70136150; PubMed=4984938;
 CC Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
 CC "Structure of porcine thyrotropin releasing hormone."
 CC Biochemistry 9:1103-1106(1970).
 CC [2]
 CC SYNTHESIS.
 CC SPECIES=Pig;
 CC MEDLINE=70039904; PubMed=4982117;
 CC Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
 CC "The identity of chemical and hormonal properties of the thyrotropin
 CC releasing hormone and pyroglutamyl-histidyl-proline amide."
 CC Biochem. Biophys. Res. Commun. 37:705-710(1969).
 CC [3]
 CC SEQUENCE.
 CC SPECIES=Sheep; TISSUE=Hypothalamus;
 CC Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,
 CC Ward D.N.;
 CC "The elucidation of the primary structure of the hypothalamic thyroid
 CC stimulating hormone releasing factor of ovine origin by means of mass
 CC spectrometry."
 CC Org. Mass Spectrom. 5:221-228 (1971).
 CC [4]
 CC SYNTHESIS.
 CC SPECIES=Sheep;
 CC MEDLINE=70163386; PubMed=4985794;
 CC Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
 CC Guillemin R.;
 CC "Characterization of ovine hypothalamic hypophysiotropic

RT TSH-releasing factor.";
 RL Nature 226:321-325 (1970).
 RN [5]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Skin;
 RX MEDLINE=76138399; PubMed=815011;
 RA Yasuhara T., Nakajima T.;
 RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin."
 RL Chem. Pharm. Bull. 23:3301-3303(1975).
 RN [6]
 RP SEQUENCE.
 RC SPECIES=N.viridescens;
 RX MEDLINE=75035605; PubMed=4214528;
 RA Grimm-Joergensen Y., McKelvy J.F.;
 RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
 viridescens) brain in vitro. Isolation and characterization of
 RT thyrotropin releasing factor."
 RL J. Neurochem. 23:471-478 (1974).
 CC -!- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
 CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
 CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
 CC PIR; A90919; RHTDFO.
 CC DR PIR; A92971; A92971.
 CC DR PIR; A93750; RSHST.
 CC KW Amidation; Pyrrolidone carboxylic acid.
 CC FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 CC FT MOD RES 3 3 AMIDATION.
 CC SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;
 CC
 CC Query Match 0.0%; Score 0; DB 1; Length 3;
 CC Best Local Similarity 0.0%; Pred. No. 0;
 CC Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 1 X 1
 CC Db 1 Q 1
 CC
 CC RESULT 4
 CC ACHI_ACHFU STANDARD; PRT; 4 AA.
 CC ID ACHI_ACHFU
 CC AC P35954;
 CC DT 01-JUN-1994 (Rel. 29, Created)
 CC DT 01-JUN-1994 (Rel. 29, Last sequence update)
 CC DT 15-JUL-1998 (Rel. 36, Last annotation update)
 CC DE Achatin-I.
 CC OS Achatina fulica (Giant African snail).
 CC OC Bukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 CC OX NCBI_TaxID=6530;
 CC [1]
 CC SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 CC STRAIN=Ferussac; TISSUE=Ganglion;
 CC MEDLINE=89273551; PubMed=2597281;
 CC Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 CC Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 CC Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
 CC "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 CC fulica Ferussac containing a D-amino acid residue."
 CC Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 CC [2]
 CC CHARACTERIZATION.
 CC STRAIN=Ferussac; TISSUE=Heart atrium;
 CC MEDLINE=91264856; PubMed=1675568;
 CC Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 CC Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
 CC "Purification of achatin-I from the atria of the African giant snail,
 CC Achatina fulica, and its possible function."
 CC Biochem. Biophys. Res. Commun. 177:847-853(1991).
 CC [3]
 CC X-RAY CRYSTALLOGRAPHY.
 CC MEDLINE=93014529; PubMed=1399265;
 CC Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,

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MM protein - protein search, using sw model

Run on: November 21, 2003, 15:20:39 ; Search time 6.4726 Seconds
(without alignments)
598.027 Million cell updates/sec

Title: US-09-010-377-3

Perfect score: 15

Sequence: 1 XXXXXXXXXXXXXXXX 15

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*

2: SP_BACTERIA:*

3: SP_FUNGI:*

4: SP_HUMAN:*

5: SP_INVERTEBRATE:*

6: SP_MAMMAL:*

7: SP_MHC:*

8: SP_ORGANELLE:*

9: SP_PHAGE:*

10: SP_PLANT:*

11: SP_RODENT:*

12: SP_VIRUS:*

13: SP_VERTEBRATE:*

14: SP_UNCLASSIFIED:*

15: SP_RVIRUS:*

16: SP_BACTERIAP:*

17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	0	0.0	4	11 Q08433	Q08433 rattus sp.
2	0	0.0	5	2 P83073	P83073 bacillus ce
3	0	0.0	5	10 Q99007	Q99007 hordeum vul
4	0	0.0	5	13 P83308	P83308 gallus gall
5	0	0.0	6	10 P82181	P82181 spinacia ol
6	0	0.0	6	10 P82541	P82541 spinacia ol
7	0	0.0	6	10 P82182	P82182 spinacia ol
8	0	0.0	7	2 Q8KMS3	Q8KMS3 klebsiella
9	0	0.0	7	2 Q47505	Q47505 escherichia
10	0	0.0	7	2 P70804	P70804 azotobacter
11	0	0.0	7	2 O50556	O50556 actinobacil
12	0	0.0	7	2 Q47477	Q47477 escherichia
13	0	0.0	7	2 Q47029	Q47029 enterobacte
14	0	0.0	7	2 P72081	P72081 nocardia la
15	0	0.0	7	2 Q54248	Q54248 streptomyc
16	0	0.0	7	2 Q8KMS9	Q8KMS9 enterobacte

17	0	0.0	7	2	Q34028	Q34028 sphingomona
18	0	0.0	7	2	Q07354	Q07354 synchococc
19	0	0.0	7	2	Q8GLI2	Q8GLI2 borrelia bu
20	0	0.0	7	2	Q8GL04	Q8GL04 borrelia bu
21	0	0.0	7	2	Q8GL00	Q8GL00 borrelia bu
22	0	0.0	7	4	Q15903	Q15903 homo sapien
23	0	0.0	7	4	Q8NH7	Q8NH7 homo sapien
24	0	0.0	7	4	Q15897	Q15897 homo sapien
25	0	0.0	7	6	Q28742	Q28742 oryctolagus
26	0	0.0	7	8	Q92214	Q92214 amblyopyrum
27	0	0.0	7	8	Q92393	Q92393 hordeum vul
28	0	0.0	7	8	Q92403	Q92403 lophopyrum
29	0	0.0	7	8	Q92427	Q92427 peridictyon
30	0	0.0	7	8	Q99182	Q99182 gnatholebia
31	0	0.0	7	8	Q92430	Q92430 aegilops ta
32	0	0.0	7	8	Q92221	Q92221 bromus iner
33	0	0.0	7	8	Q98866	Q98866 spinacia ol
34	0	0.0	7	8	Q92425	Q92425 pseudoroegn
35	0	0.0	7	8	Q92381	Q92381 hordeum bra
36	0	0.0	7	8	Q92387	Q92387 henardia p
37	0	0.0	7	8	Q92210	Q92210 agropyron c
38	0	0.0	7	8	Q92440	Q92440 thinopyrum
39	0	0.0	7	8	Q92218	Q92218 australopyr
40	0	0.0	7	8	Q92390	Q92390 heteranthel
41	0	0.0	7	8	Q92372	Q92372 haynaldia v
42	0	0.0	7	8	Q92442	Q92442 taeniatheir
43	0	0.0	7	8	Q92226	Q92226 crithopsis
44	0	0.0	7	8	Q8MPY6	Q8MPY6 taraxacum (
45	0	0.0	7	8	Q95945	Q95945 saccharomyC

ALIGNMENTS

RESULT 1

Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -.
KW Transferase.
FT NON TER 1
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 0.0%; Score 0; DB 11; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 N 1

RESULT 2

P83073 PRELIMINARY; PRT; 5 AA.
AC P83073;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)

01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 88 kDa protein (Fragment).
 Bacillus cereus.
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=1396;
 [1]
 SEQUENCE.
 STRAIN=NCIMB 11796;
 BROWN N., DOWDS B.C.A.;
 Submitted (JUL-2001) to the SWISS-PROT data bank.
 NON_TER 5
 SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;
 Query Match 0.0%; Score 0; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 4 T 4
 RESULT 3
 Q99007 PRELIMINARY; PRT; 5 AA.
 ID Q99007;
 AC Q99007;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Alpha amylase (Fragment).
 GN AMY1 GENE.
 OS Hordeum vulgare (Barley).
 OS Eukaryota; Viridiplantae;
 OC Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 NCBI_TaxID=4513;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=91329704; PubMed=1831085;
 JACOBSEN J.V., CLOSE T.J.;
 "Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley aleurone layers."
 Plant Mol. Biol. 16:713-721(1991).
 EMBL; X54643; CAA38455.1; -.
 NON_TER 5
 SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;
 Query Match 0.0%; Score 0; DB 10; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 2 A 2
 RESULT 4
 P83308 PRELIMINARY; PRT; 5 AA.
 ID P83308;
 AC P83308;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE FMRamide-like neuropeptide (IPURF-amide).
 OS Gallus gallus (Chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 NCBI_TaxID=9031;
 [1]
 SEQUENCE, AND SYNTHESIS.

RC TISSUE=Brain;
 RX PubMed=6137771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Cayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 RT antibodies to FMRamide."
 RL Nature 305:328-330(1983).
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;
 Query Match 0.0%; Score 0; DB 13; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 1 L 1
 RESULT 5
 P82181 PRELIMINARY; PRT; 6 AA.
 ID P82181;
 AC P82181;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 NCBI_TaxID=3562;
 [1]
 SEQUENCE.
 RC STRAIN=cv. ALVARO; TISSUE=Leaf;
 RX MEDLINE=20435798; PubMed=10874046;
 YAMAGUCHI K., SUBRAMANIAN A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR001790; Ribosomal_L10.
 DR InterPro; IPR002363; Ribosomal_L10eub.
 DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 NON_TER 6
 SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
 Query Match 0.0%; Score 0; DB 10; Length 6;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 1 A 1
 RESULT 6
 P82541 PRELIMINARY; PRT; 6 AA.
 ID P82541;
 AC P82541;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
 OS Spinacia oleracea (Spinach).

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M protein - protein search, using sw model

un on: November 21, 2003, 15:19:18 ; Search time 16.6438 Seconds
(without alignments)
286.100 Million cell updates/sec

title: US-09-010-377-4
perfect score: 30
sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 30

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 1107863 seqs, 158726573 residues

total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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11: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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19: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
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22: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	0.0	1	20 AAY46652	Immunogenic peptid
2	0	0.0	1	22 ABB56870	Human SNP related
3	0	0.0	1	22 ABB68809	Drosophila melanog
4	0	0.0	1	22 ABB66810	Novel human diagno
5	0	0.0	1	22 ABB02941	Human peptide #918
6	0	0.0	1	22 AAM97643	Human peptide #110
7	0	0.0	1	22 AAM97834	Human peptide #124
8	0	0.0	1	22 AAM97974	Human peptide #162
9	0	0.0	1	22 AAM98354	

10	0	0.0	1	22 AAM98447	Human peptide #172
11	0	0.0	1	22 AAM53218	Human nonconservat
12	0	0.0	1	22 AAM53219	Human nonconservat
13	0	0.0	1	22 AAM53290	Human nonconservat
14	0	0.0	1	22 AAM53291	Human nonconservat
15	0	0.0	1	22 AAM53328	Human nonconservat
16	0	0.0	1	22 AAM53329	Human nonconservat
17	0	0.0	1	22 AAM45230	H11 binding site c
18	0	0.0	1	22 AAG99966	ERA binding domain
19	0	0.0	1	22 AAG99983	ERA binding domain
20	0	0.0	1	22 AAG99987	ERA binding domain
21	0	0.0	1	22 AAG99988	ERA binding domain
22	0	0.0	1	22 AAM00010	ERA binding domain
23	0	0.0	1	22 AAM00011	ERA binding domain
24	0	0.0	1	22 AAM00013	ERA binding domain
25	0	0.0	1	22 AAM00016	Human SNP associat
26	0	0.0	1	22 AAG98026	Human SNP associat
27	0	0.0	1	22 AAG98134	Thyrotropin releas
28	0	0.0	1	22 AAB91029	Endothelins and re
29	0	0.0	1	22 AAB91546	Opioid peptide SEQ
30	0	0.0	1	22 AAB91655	Opioid peptide SEQ
31	0	0.0	1	22 AAB91739	Apoptosis related
32	0	0.0	1	22 AAB91892	Polypeptide SEQ ID
33	0	0.0	1	22 AAB92150	Miscellaneous pept
34	0	0.0	1	22 AAB92392	Helicobacter pylor
35	0	0.0	1	23 ABUS1078	Helicobacter pylor
36	0	0.0	1	23 ABUS1919	Helicobacter pylor
37	0	0.0	1	23 ABUS2012	Helicobacter pylor
38	0	0.0	1	23 ABUS2118	Human novel secret
39	0	0.0	1	23 ABG95255	Human novel secret
40	0	0.0	1	23 ABG95471	Human P-glycoprote
41	0	0.0	1	23 ABG93483	Human P-glycoprote
42	0	0.0	1	23 ABG93484	Human P-glycoprote
43	0	0.0	1	23 ABG93489	Human P-glycoprote
44	0	0.0	1	23 ABG93491	Human P-glycoprote
45	0	0.0	1	23 ABG93499	Human P-glycoprote

ALIGNMENTS

RESULT 1
AAY46652
ID AAY46652 standard; Peptide; 1 AA.
XX
AC AAY46652;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #1263.
XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
XX Synthetic.
OS Homo sapiens.
XX
PN WO9945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX
XX WPI; 1999-551214/46.

XX
PT New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -
XX
PS Claim 1; Page 80; 150pp; English.
XX
XX
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
CC are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The
CC polynucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.
XX
SQ Sequence 1 AA;

Query Match 0.0%; Score 0; DB 20; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 Y 1

RESULT 2
ABB56870
ID ABB56870 standard; Peptide; 1 AA.
XX
XX ABB56870;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human SNP related amino acid sequence SEQ ID NO:1435.
XX
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein.
XX
XX Homo sapiens.
XX
XX WO200138586-A2.
XX
XX 31-MAY-2001.
XX
XX 22-NOV-2000; 2000WO-US32311.
XX
XX 24-NOV-1999; 99US-0167383.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX
XX WPI; 2001-355949/37.
XX
XX Isolated human nucleic acids comprising one or more single nucleotide
XX polymorphisms, useful for treating a subject suffering from a
PT pathology, e.g. autoimmune diseases, ascribed to the presence of a
PT

PT sequence polymorphism -
XX Claim 1; Page 666; 674pp; English.
XX
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the
CC polymorphic protein within appropriate physiological samples).
XX
SQ Sequence 1 AA;

Query Match 0.0%; Score 0; DB 22; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 S 1

RESULT 3
ABB66809
ID ABB66809 standard; Protein; 1 AA.
XX
XX ABB66809;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 27219.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL10912.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Disclosure; SEQ ID NO 27219; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of

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OM protein - protein search, using sw model

Run on: November 21, 2003, 15:21:54 ; Search time 5.65068 Seconds
(without alignments)
224.632 Million cell updates/sec

Title: US-09-010-377-4
Perfect score: 30
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXXX 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	0	0.0	1	1	US-07-820-154A-12
2	0	0.0	1	1	US-07-791-213D-24
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4	0	0.0	1	1	US-08-174-365A-57
5	0	0.0	1	1	US-07-789-913-23
6	0	0.0	1	1	US-07-789-913-25
7	0	0.0	1	1	US-08-049-794-23
8	0	0.0	1	1	US-08-049-794-25
9	0	0.0	1	1	US-08-433-037-12
10	0	0.0	1	1	US-08-448-606-4
11	0	0.0	1	1	US-07-869-933-16
12	0	0.0	1	1	US-08-293-150A-24
13	0	0.0	1	1	US-08-293-150A-40
14	0	0.0	1	1	US-08-496-847-23
15	0	0.0	1	1	US-08-496-847-25
16	0	0.0	1	2	US-08-742-774-23
17	0	0.0	1	2	US-08-742-774-25
18	0	0.0	1	2	US-08-675-354-23
19	0	0.0	1	2	US-08-675-354-25
20	0	0.0	1	2	US-08-575-554A-12
21	0	0.0	1	2	US-08-965-918-23
22	0	0.0	1	2	US-08-965-918-25
23	0	0.0	1	2	US-09-138-439-23
24	0	0.0	1	2	US-09-138-439-25
25	0	0.0	1	3	US-08-480-640A-12
26	0	0.0	1	3	US-08-613-400A-23
27	0	0.0	1	3	US-08-613-400A-25

28	0	0.0	1	3	US-08-801-092-10	Sequence 10, Appl
29	0	0.0	1	3	US-08-801-092-17	Sequence 17, Appl
30	0	0.0	1	3	US-08-801-092-24	Sequence 24, Appl
31	0	0.0	1	3	US-08-801-092-31	Sequence 31, Appl
32	0	0.0	1	3	US-08-801-092-38	Sequence 38, Appl
33	0	0.0	1	3	US-08-801-092-45	Sequence 45, Appl
34	0	0.0	1	3	US-09-298-017-23	Sequence 23, Appl
35	0	0.0	1	3	US-09-298-017-25	Sequence 25, Appl
36	0	0.0	1	3	US-08-295-802-12	Sequence 12, Appl
37	0	0.0	1	3	US-09-392-979A-23	Sequence 23, Appl
38	0	0.0	1	3	US-09-392-979A-25	Sequence 25, Appl
39	0	0.0	1	3	US-09-103-663-16	Sequence 16, Appl
40	0	0.0	1	3	US-08-488-237A-12	Sequence 12, Appl
41	0	0.0	1	3	US-09-117-927-5	Sequence 5, Appl
42	0	0.0	1	4	US-08-375-992A-12	Sequence 12, Appl
43	0	0.0	1	4	US-09-315-113-10	Sequence 10, Appl
44	0	0.0	1	4	US-09-315-113-17	Sequence 17, Appl
45	0	0.0	1	4	US-09-315-113-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-07-820-154A-12
; Sequence 12, Application US/07820154A
; Patent No. 5382425
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; APPLICANT: Junker M.S., David E
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/820,154A
; FILING DATE: 19920113
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-820-154A-12

Query Match 0.0%; Score 0; DB 1; length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 V 1

RESULT 2
US-07-791-213D-24

; Sequence 24, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-791-213D-24

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 C 1

RESULT 3
US-07-791-213D-40
; Sequence 40, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States

; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-791-213D-40

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 C 1

RESULT 4
US-08-174-365A-57
; Sequence 57, Application US/08174365A
; Patent No. 5478809
; GENERAL INFORMATION:
; APPLICANT: Seiichi TANIDA et al.
; TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,365A
; FILING DATE: December 28, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 15:27:54 ; Search time 11.1986 Seconds
(without alignments)
489.058 Million cell updates/sec

Title: US-09-010-377-4

Perfect score: 30

Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXXXXX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 18259486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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15	0	0.0	1	10	US-09-982-172-86

16	0	0.0	1	10	US-09-982-172-93	Sequence 93, Appl
17	0	0.0	1	10	US-09-982-172-95	Sequence 95, Appl
18	0	0.0	1	10	US-09-982-172-106	Sequence 106, App
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22	0	0.0	1	10	US-09-982-172-148	Sequence 126, App
23	0	0.0	1	10	US-09-982-172-148	Sequence 148, App
24	0	0.0	1	10	US-09-982-172-155	Sequence 149, App
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26	0	0.0	1	10	US-09-982-172-172	Sequence 160, App
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28	0	0.0	1	10	US-09-982-172-175	Sequence 173, App
29	0	0.0	1	10	US-09-982-172-189	Sequence 175, App
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34	0	0.0	1	10	US-09-982-172-211	Sequence 200, App
35	0	0.0	1	11	US-09-809-391-395	Sequence 211, App
36	0	0.0	1	11	US-09-809-391-395	Sequence 395, App
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38	0	0.0	1	12	US-10-299-619-4	Sequence 19, Appl
39	0	0.0	1	12	US-10-061-607A-28	Sequence 4, Appl
40	0	0.0	1	12	US-10-061-607A-29	Sequence 28, Appl
41	0	0.0	1	12	US-10-061-607A-35	Sequence 35, Appl
42	0	0.0	1	12	US-09-882-171-395	Sequence 395, App
43	0	0.0	1	12	US-09-882-171-611	Sequence 611, App
44	0	0.0	1	12	US-10-104-307-7	Sequence 7, Appl
45	0	0.0	1	12	US-10-104-307-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-09-909-348-4
; Sequence 4, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; NAME/KEY: VARIANT
; LOCATION: (1)...(14)
; OTHER INFORMATION: Xaa at position six is Glu or Gin
; OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or
US-09-909-348-4

Query Match 0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 V 1

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RESULT 2
US-09-982-172-3
; Sequence 3, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-3
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Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 K 1
RESULT 3
US-09-982-172-4
; Sequence 4, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-4
Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 K 1
RESULT 4
US-09-982-172-9
; Sequence 9, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-9
Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 K 1
RESULT 5
US-09-982-172-11
; Sequence 11, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-11
Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 K 1
RESULT 6
US-09-982-172-19
; Sequence 19, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-19
Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 K 1
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2003, 15:21:14 ; Search time 5.54795 Seconds
(without alignments)
520.023 Million cell updates/sec

Title: US-09-010-377-4
Perfect score: 30
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	0	0.0	3	3 RHTDIO	thyroliberin - Bom
2	0	0.0	3	3 RHPGT	thyroliberin - pig
3	0	0.0	3	3 RSHST	thyroliberin - she
4	0	0.0	3	3 A92371	thyroliberin - eas
5	0	0.0	3	3 GKHU	growth-modulating
6	0	0.0	3	3 A60898	bursin - chicken
7	0	0.0	3	3 A23751	spinal cord peptid
8	0	0.0	3	3 B23751	spinal cord peptid
9	0	0.0	3	3 A33802	thyrotropin-releas
10	0	0.0	3	3 A22565	R-phycoerythrin al
11	0	0.0	3	3 PQ0010	angiotensin-conver
12	0	0.0	3	3 S13894	histidinol dehydro
13	0	0.0	3	3 A43391	TRH-like tripeptid
14	0	0.0	3	3 E37196	bradykinin-potentl
15	0	0.0	3	3 F37196	gene p20K protein
16	0	0.0	3	3 I50412	bradykinin-potentl
17	0	0.0	3	3 PT0636	T-cell receptor be
18	0	0.0	3	3 PT0578	T-cell receptor be
19	0	0.0	3	3 PT0571	T-cell receptor be
20	0	0.0	3	3 PT0622	tyrosine protein k
21	0	0.0	3	3 I78890	blood cell protein
22	0	0.0	3	3 S68328	cytochrome-c oxida
23	0	0.0	3	3 T13892	antho-rfamide neur
24	0	0.0	4	1 ECXAA	thyroglobulin - do
25	0	0.0	4	2 S18401	phagocytosis-stimu
26	0	0.0	4	2 A02147	tyrosine-melanocyt
27	0	0.0	4	2 A32039	cardioexcitatory n
28	0	0.0	4	2 ECNK	carbon-monoxide de
29	0	0.0	4	2 PL0140	

30	0	0.0	4	2 PL0146	carbon-monoxide de
31	0	0.0	4	2 A37832	phenol 2-monooxyge
32	0	0.0	4	2 A48360	gamma subunit of p
33	0	0.0	4	2 I40697	biotin A - Citroba
34	0	0.0	4	2 A61300	22K superhelical D
35	0	0.0	4	2 I57745	D-mannosate hydrol
36	0	0.0	4	2 A41890	protein D - Escher
37	0	0.0	4	2 S43014	hypothetical prote
38	0	0.0	4	2 D41654	hypothetical prote
39	0	0.0	4	2 B43848	cell surface adhes
40	0	0.0	4	2 I40505	hypothetical prote
41	0	0.0	4	2 I40870	phospholipase C (E
42	0	0.0	4	2 I40804	endoglucanase F -
43	0	0.0	4	2 T46627	hypothetical prote
44	0	0.0	4	2 S53508	starvation-induced
45	0	0.0	4	2 S17255	ribosomal protein

ALIGNMENTS

RESULT 1

RHTDIO
thyroliberin - Bombina orientalis
C;Species: Bombina orientalis
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A90919; A01415
R;Yasuhara, T.; Nakajima, T.
Chem. Pharm. Bull. 23, 3301-3303, 1975
A;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.
A;Reference number: A90919; MUID:76138399; PMID:815011
A;Accession: A90919
A;Molecule type: protein
A;Residues: 1-3 <YAS>
C;Superfamily: thyroliberin precursor
C;Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 Q 1

RESULT 2

RHPGT
thyroliberin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A01415
R;Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.
Biochemistry 9, 1103-1106, 1970
A;Title: Structure of porcine thyrotropin releasing hormone.
A;Reference number: A90560; MUID:70136150; PMID:4984938
A;Accession: A01415
A;Molecule type: protein
A;Residues: 1-3 <NAL>
R;Boiler, J.; Enzmann, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.
Biochem. Biophys. Res. Commun. 37, 705-710, 1969
A;Title: The identity of chemical and hormonal properties of the thyrotropin releasing hc
A;Reference number: A90167; MUID:70039904; PMID:4982117
A;Contents: annotation
A;Note: biological activities and Rf values (in 17 chromatographic systems) of the synthe
C;Superfamily: thyroliberin precursor
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 Q 1

RESULT 3
RHSH
thyroliberin - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A93750; A01415
R:Desiderio J.R., D.M.; Burgus, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
Org. Mass Spectrom. 5, 221-228, 1971
A:Title: The elucidation of the primary structure of the hypothalamic thyroïd stimulin
A:Reference number: A93750
A:Accession: A93750
A:Molecule type: protein
A:Residues: 1-3 <DES>
R:Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.
Nature 226, 321-325, 1970
A:Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.
A:Reference number: A93161; MUID:70163386; PMID:4985794
A:Contents: annotation
A:Note: physicochemical characteristics and biological activities of the natural and synthetic thyroliberin precursor
C:Superfamily: thyroliberin precursor
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 Q 1

RESULT 4
A92971
thyroliberin - eastern newt (tentative sequence)
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A92971; A01415
R:Grimm-Jorgensen, Y.; McKelvy, J.F.
J. Neurochem. 23, 471-478, 1974
A:Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain
A:Reference number: A92971; MUID:75035605; PMID:4214528
A:Accession: A92971
A:Molecule type: protein
A:Residues: 1-3 <GRI>
A:Note: a peptide with the chromatographic and electrophoretic characteristics of thyroliberin, or glutamic acid
C:Superfamily: thyroliberin precursor
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 Q 1

RESULT 5
GKHU
growth-modulating peptide - human

C:Species: Homo sapiens (man)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A01421
R:Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A:Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A:Reference number: A01421; MUID:77162369; PMID:858356
A:Accession: A01421
A:Molecule type: protein
A:Residues: 1-3 <SCH>
A:Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit growth-modulating peptide - human
C:Superfamily: unassigned animal peptides

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 G 1

RESULT 6
A60898
bursin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A60898
R:Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 231, 997-999, 1986
A:Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of the chicken
A:Reference number: A60898; MUID:86122916; PMID:3484838
A:Accession: A60898
A:Molecule type: protein
A:Residues: 1-3 <AUD>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; hormone
F:3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 K 1

RESULT 7
A23751
spinal cord peptide SCP-4 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A23751
R:Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985
A:Reference number: A23751; MUID:85250425; PMID:4015098
A:Accession: A23751
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <HSI>
C:Superfamily: unassigned animal peptides

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 Q 1

RESULT 8

GenCore version 5.1.6
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DM protein - protein search, using sw model

Run on: November 21, 2003, 15:20:03 ; Search time 2.97945 Seconds
(without alignments)
473.510 Million cell updates/sec

Title: US-09-010-377-4
Perfect score: 30
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	0.0	3	1 GRWM_HUMAN	P01157 homo sapien
2	0	0.0	3	1 LUXE_VIBFI	P24272 vibrio fisc
3	0	0.0	3	1 THYL_PIG	P01151 sus scrofa
4	0	0.0	4	1 ACHI_ACHF	P35904 achatina fu
5	0	0.0	4	1 DCML_PSECH	P19916 pseudomonas
6	0	0.0	4	1 DCMS_PSECH	P19918 pseudomonas
7	0	0.0	4	1 EOSI_HUMAN	P02731 homo sapien
8	0	0.0	4	1 FAR3_HIRME	P42562 hirudo medi
9	0	0.0	4	1 FAR4_HIRME	P42563 hirudo medi
10	0	0.0	4	1 FFKA_ANTEL	P58705 anthopleura
11	0	0.0	4	1 FLRF_HIRME	P42561 hirudo medi
12	0	0.0	4	1 FLRN_ANTEL	P58707 anthopleura
13	0	0.0	4	1 FMRF_MACNI	P01162 macrocallis
14	0	0.0	4	1 FVRI_ANTEL	P58706 anthopleura
15	0	0.0	4	1 OCPI_OCTMI	P58648 octopus min
16	0	0.0	4	1 OCB3_OCTMI	P58649 octopus min
17	0	0.0	4	1 RM01_YEAST	P36515 saccharomyc
18	0	0.0	4	1 TUFT_HUMAN	P01858 homo sapien
19	0	0.0	5	1 ALI4_CARMA	P81817 carcinus ma
20	0	0.0	5	1 B1OA_CITFR	P13071 citrobacter
21	0	0.0	5	1 B1OB_CITFR	P12997 citrobacter
22	0	0.0	5	1 BPPT_BOTIN	P30425 bothrops in
23	0	0.0	5	1 E1O3_LITRU	P82099 litoria rub
24	0	0.0	5	1 E1O4_LITRU	P82100 litoria rub
25	0	0.0	5	1 FARP_ARTTR	P41853 artiposthi
26	0	0.0	5	1 PRCT_PARMA	P81864 pardachirus
27	0	0.0	5	1 PRCT_PPRAM	P01373 periplaneta
28	0	0.0	5	1 PSK_DAUCA	P58361 daucus caro
29	0	0.0	5	1 RE11_LITRU	P82070 litoria rub
30	0	0.0	5	1 RE21_LITRU	P82071 litoria rub
31	0	0.0	5	1 RE31_LITRU	P82072 litoria rub
32	0	0.0	5	1 RE32_LITRU	P82073 litoria rub
33	0	0.0	5	1 SUGA_ACHDO	P19991 acheta dome

34 0 0.0 5 1 TPIS_CANFA P54714 canis famil
35 0 0.0 5 1 TRM3_ECOLI P13973 escherichia
36 0 0.0 5 1 UC22_MAIZE P80628 zea mays (m
37 0 0.0 5 1 UF01_MOUSE P38639 mus musculu
38 0 0.0 5 1 UXA4_CHLTR P38005 chlamydia t
39 0 0.0 6 1 ACPH_RABIT P25154 oryctolagus
40 0 0.0 6 1 ASP2_LACSN P82655 lactobacill
41 0 0.0 6 1 CIP1_MYTED P13736 mytilus edu
42 0 0.0 6 1 CIP2_MYTED P13737 mytilus edu
43 0 0.0 6 1 E1O1_LITRU P82096 litoria rub
44 0 0.0 6 1 FARP_MONEX P41966 moniezia ex
45 0 0.0 6 1 LOK1_LOCM1 P41491 locusta mig

ALIGNMENTS

RESULT 1

ID GRWM_HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RT Schlesinger D.H., Pickart L., Thaler M.M.;
RA "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experimentia 33:324-325(1977).
CC -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR GO; GO:0001558; P:regulation of cell growth; NAS.
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 G 1

RESULT 2

ID LUXE_VIBFI STANDARD; PRT; 3 AA.
AC P24272;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
protein synthetase) (Fragment).
GN LUXE.
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
NCBI_TaxID=668;
RN [1]_SEQUENCE FROM N.A.
RX MEDLINE=91072226; PubMed=2254256;
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
site for the lux operon."
RL J. Bacteriol. 172:6797-6802(1990).
CC -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS

```

CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC an acyl-protein thioester.
CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M62812; -; NOT ANNOTATED_CDS.
CC DR LUMINESCENCE; Ligase.
CC KW NON TER 1 1
CC FT SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;
CC SQ

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Query Match 0.0%; Score 0; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
 Db 1 1 1

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RESULT 3
THYL PIG
ID THYL PIG STANDARD; PRT; 3 AA.
AC F01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
OS Sus scrofa (Pig),
OS Ovis aries (Sheep),
OS Bombina orientalis (Oriental fire-bellied toad), and
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 9940, 8346, 8316;
[1]_TaxID=9823, 9940, 8346, 8316;
SEQUENCE.
SP SPECIES=Pig; TISSUE=Hypothalamus;
RC MEDLINE=70136150; PubMed=4984938;
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
RT "Structure of porcine thyrotropin releasing hormone.";
RL Biochemistry 9:1103-1106(1970).
RN [2]
RP SYNTHESIS.
RC SPECIES=Pig;
RC MEDLINE=70039904; PubMed=4982117;
RX Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
RA "The identity of chemical and hormonal properties of the thyrotropin
RT releasing hormone and pyroglutamyl-histidyl-proline amide.";
RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=Sheep; TISSUE=Hypothalamus;
RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,
RD Ward D.N.;
RT "The elucidation of the primary structure of the hypothalamic thyroid
RT stimulating hormone releasing factor of ovine origin by means of mass
RT spectrometry.";
RL Org. Mass Spectrom. 5:221-228(1971).
RN [4]
RP SYNTHESIS.
RC SPECIES=Sheep;
RC MEDLINE=70163386; PubMed=4985794;
RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
RD Guillemin R.;
RT "Characterization of ovine hypothalamic hypophysiotropic

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RT TSH-releasing factor.";
RL Nature 226:321-325(1970).
RN [5]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Skin;
RX MEDLINE=76138399; PubMed=815011;
RA Yasuhara T., Nakajima T.;
RT "Letter: Occurrence of Pyl-His-Pro-NH2 in the frog skin.";
RL Chem. Pharm. Bull. 23:3301-3303(1975).
RN [6]
RP SEQUENCE.
RC SPECIES=N.viridescens;
RX MEDLINE=75035605; PubMed=4214528;
RA Grimm-Joergensen Y., McKelvy J.F.;
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
RT viridescens) brain in vitro. Isolation and characterization of
RT thyrotropin releasing factor.";
RL J. Neurochem. 23:471-478(1974).
CC -!- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
CC PIR; A90919; RHTDIO.
DR PIR; A92971; A92971.
DR PIR; A93750; RSHST.
KW Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 3 3 AMIDATION.
SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

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Query Match 0.0%; Score 0; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
 Db 1 Q 1

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RESULT 4
ACH1 ACHFU
ID ACH1 ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Achatin-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
[1]
RN SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RP STRAIN=Perussac; TISSUE=Ganglion;
RC MEDLINE=89273551; PubMed=2597281;
RX Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RA "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT fulica Perussac containing a D-amino acid residue.";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RN CHARACTERIZATION.
RP STRAIN=Perussac; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT "Purification of achatin-I from the atria of the African giant snail,
RT Achatina fulica, and its possible function.";
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
RN X-RAY CRYSTALLOGRAPHY.
RP MEDLINE=93014529; PubMed=1399265;
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,

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OM protein - protein search, using sw model

Run on: November 21, 2003, 15:20:39 : Search time 12.9452 Seconds
(without alignments)
598.027 Million cell updates/sec

Title: US-09-010-377-4
Perfect score: 30
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXXXXXX 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	%	Query Match	Length	ID	Description
1	0	0.0	0	4	11 Q08433	Q08433 rattus sp.
2	0	0.0	5	2	P83073	P83073 bacillus ce
3	0	0.0	5	10	Q99007	Q99007 hordeum vul
4	0	0.0	5	13	P83308	P83308 gallus gall
5	0	0.0	6	10	P82181	P82181 spinacia ol
6	0	0.0	6	10	P82541	P82541 spinacia ol
7	0	0.0	6	10	P82182	P82182 spinacia ol
8	0	0.0	7	2	Q8KMS3	Q8KMS3 klebsiella
9	0	0.0	7	2	Q47505	Q47505 escherichia
10	0	0.0	7	2	P70804	P70804 azotobacter
11	0	0.0	7	2	O50556	O50556 acinetobact
12	0	0.0	7	2	Q47477	Q47477 escherichia
13	0	0.0	7	2	Q47029	Q47029 enterobacte
14	0	0.0	7	2	P72081	P72081 nocardia la
15	0	0.0	7	2	Q54248	Q54248 streptomyce
16	0	0.0	7	2	Q8KMS9	Q8KMS9 enterobacte

17	0	0.0	7	2	O34028	O34028 sphingomona
18	0	0.0	7	2	O07354	O07354 synechococc
19	0	0.0	7	2	Q8GL12	Q8GL12 borrelia bu
20	0	0.0	7	2	Q8GL04	Q8GL04 borrelia bu
21	0	0.0	7	2	Q8GL00	Q8GL00 borrelia bu
22	0	0.0	7	4	Q15903	Q15903 homo sapien
23	0	0.0	7	4	Q8NH7	Q8NH7 homo sapien
24	0	0.0	7	4	Q15897	Q15897 homo sapien
25	0	0.0	7	6	Q28742	Q28742 oryctolagus
26	0	0.0	7	8	P92214	P92214 amblyopium
27	0	0.0	7	8	P92393	P92393 hordeum vul
28	0	0.0	7	8	P92403	P92403 lophopyrum
29	0	0.0	7	8	P92427	P92427 peridictyon
30	0	0.0	7	8	O99182	O99182 gnatholebia
31	0	0.0	7	8	P92430	P92430 aegilops ta
32	0	0.0	7	8	P92221	P92221 bromus iner
33	0	0.0	7	8	O98866	O98866 spinacia ol
34	0	0.0	7	8	P92425	P92425 pseudoroegn
35	0	0.0	7	8	P92381	P92381 hordeum bra
36	0	0.0	7	8	P92387	P92387 henrardia p
37	0	0.0	7	8	P92210	P92210 agropyron c
38	0	0.0	7	8	P92440	P92440 thinopyrum
39	0	0.0	7	8	P92218	P92218 australopyr
40	0	0.0	7	8	P92390	P92390 heteranthe
41	0	0.0	7	8	P92372	P92372 haynaldia v
42	0	0.0	7	8	P92442	P92442 taeniatheru
43	0	0.0	7	8	P92226	P92226 crithopsis
44	0	0.0	7	8	Q8MFY6	Q8MFY6 taraxacum (
45	0	0.0	7	8	Q95945	Q95945 saccharomyc

ALIGNMENTS

RESULT 1

Q08433 ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat."
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -.
KW Transferase.
FT NON_TER 1 1
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 0.0%; Score 0; DB 11; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 N 1

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P83073 ID P83073 PRELIMINARY; PRT; 5 AA.
AC P83073;
DT 01-OCT-2001 (TRENBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE 88 kDa protein (Fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=1396;
 (1) _RN
 RP SEQUENCE
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 FT NON TER 5
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;
 QY Query Match 0.0%; Score 0; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 4 T 4
 RESULT 3
 Q99007 PRELIMINARY; PRT; 5 AA.
 ID AC Q99007;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Alpha amylase (Fragment).
 GN AMY1 GENE.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 NCBI_TaxID=4513;
 (1) _RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley aleurone layers."
 RT Plant Mol. Biol. 16:713-721(1991).
 EN EMBL; X54643; CAA38455.1; --
 FT NON TER 5
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;
 QY Query Match 0.0%; Score 0; DB 10; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 2 A 2
 RESULT 4
 P83308 PRELIMINARY; PRT; 5 AA.
 ID AC P83308;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE FMRFamide-like neuropeptide (IPLRF-amide).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianinae; Gallus.
 NCBI_TaxID=9031;
 (1) _RN
 RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Brain;
 RX PubMed=6137771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by antibodies to FMRFamide."
 RL Nature 305:328-330(1983).
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;
 QY Query Match 0.0%; Score 0; DB 13; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 1 L 1
 RESULT 5
 P82181 PRELIMINARY; PRT; 6 AA.
 ID AC P82181;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 NCBI_TaxID=3562;
 (1) _RN
 RP SEQUENCE.
 RC STRAIN=cv. ALVARO; TISSUE=Leaf;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR001790; Ribosomal L10.
 DR InterPro; IPR002363; Ribosomal_L10sub.
 DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON TER 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB0000 CRC64;
 QY Query Match 0.0%; Score 0; DB 10; Length 6;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 1 A 1
 RESULT 6
 P82541 PRELIMINARY; PRT; 6 AA.
 ID AC P82541;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
 OS Spinacia oleracea (Spinach).

GenCore version 5.1.6
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Protein - protein search, using sw model

Run on: November 21, 2003, 15:19:18 ; Search time 9.9863 Seconds
(without alignments)
286.100 Million cell updates/sec

Title: US-09-010-377-5
Perfect score: 35
Sequence: 1 XXXXXXXPVFXXXXXX 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	60.0	4	17 AAR92613	VLA-4 binding pept
2	21	60.0	5	17 AAR92607	VLA-4 binding pept
3	21	60.0	6	17 AAR92604	VLA-4 binding pept
4	21	60.0	6	17 AAR92614	VLA-4 binding pept
5	21	60.0	6	17 AAR92531	VLA-4 binding pept
6	21	60.0	7	17 AAR92599	VLA-4 binding pept
7	21	60.0	8	17 AAR92602	VLA-4 binding pept
8	21	60.0	9	17 AAR92610	VLA-4 binding pept
9	21	60.0	9	22 ABP21019	HIV A03 motif pol

10	21	60.0	10	17 AAR92598	VLA-4 binding pept
11	21	60.0	10	17 AAR92573	VLA-4 binding pept
12	21	60.0	10	21 AAY56008	Mucor hiemalis end
13	21	60.0	10	22 ABP21021	HIV A03 motif pol
14	21	60.0	11	17 AAR92563	VLA-4 binding pept
15	21	60.0	11	17 AAR92601	VLA-4 binding pept
16	21	60.0	11	22 ABP21023	HIV A03 motif pol
17	21	60.0	12	21 AAY93861	Reactive peptide w
18	21	60.0	13	22 AAB49917	Human P-glycoprote
19	21	60.0	13	22 AAB49920	Human P-glycoprote
20	21	60.0	14	23 ABG93568	Human P-glycoprote
21	21	60.0	14	23 ABG93704	Human P-glycoprote
22	21	60.0	14	23 ABP47053	Human Blys binding
23	21	60.0	15	23 ABP58590	Human cysteine swi
24	21	60.0	15	23 AAO14991	Human synaptophys
25	21	60.0	18	21 AAY91149	Modified HBV surfa
26	21	60.0	18	23 ABG68218	Hepatitis B virus
27	21	60.0	19	21 AAB34287	Human secreted pro
28	21	60.0	22	21 AAY65274	Human 5' EST relat
29	21	60.0	25	24 ABJ18878	Human Bcl-XL-bindi
30	21	60.0	27	22 AAM95657	Human reproductive
31	21	60.0	28	21 AAB45151	Human secreted pro
32	21	60.0	30	21 AAY91189	Modified HBV surfa
33	21	60.0	32	22 ABG48897	Human liver peptid
34	21	60.0	32	22 ABG53276	Human liver peptid
35	21	60.0	32	22 ABB28892	Peptide #1543 enco
36	21	60.0	32	22 ABB34068	Peptide #1574 enco
37	21	60.0	32	22 ABB38450	Peptide #5956 enco
38	21	60.0	32	22 ABB19508	Protein #1507 enco
39	21	60.0	32	22 ABB23617	Protein #5616 enco
40	21	60.0	32	22 AAM54850	Human brain expres
41	21	60.0	32	22 AAM59061	Human brain expres
42	21	60.0	32	22 AAM67232	Human bone marrow
43	21	60.0	32	22 AAM71594	Human bone marrow
44	21	60.0	32	22 AAM15077	Peptide #1511 enco
45	21	60.0	32	22 AAM27525	Peptide #1562 enco

ALIGNMENTS

RESULT 1
AAR92613
ID AAR92613 standard; peptide; 4 AA.

XX AAR92613;
XX
XX 10-SEP-1996 (first entry)
XX
XX VLA-4 binding peptide #73.

XX VLA-4; inhibitor; binding peptide; leucocyte adhesion; CD49d/CD29; CDR;
KW alpha4beta1 integrin; VCAM-1; endothelial cell; antibody; meningitis;
KW complementarity determining region; inflammatory brain disorder; therapy;
KW multiple sclerosis; encephalitis; Alzheimer's disease; atherosclerosis;
KW AIDS dementia; diabetes; inflammatory bowel disease; tumour metastases;
KW rheumatoid arthritis; transplant rejection; myocardial ischaemia; asthma.

XX Synthetic.
XX OS
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "acetylated"

XX WO9601644-A1.
XX
XX 25-JAN-1996.
XX
XX 10-JUL-1995; 95WO-US08516.
XX
XX 06-JUN-1995; 95US-0467580.
XX 11-JUL-1994; 94US-0273055.
XX

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08516
FILING DATE: 10-JUL-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,055
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 002010-008
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-3620
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-08516-82

Query Match 60.0%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
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Db 1 PVSF 4

RESULT 3
US-08-467-580-75
; Sequence 75, Application US/08467580B
; Patent No. 6001809
; GENERAL INFORMATION:
; APPLICANT: Thorsett, Eugene D
; APPLICANT: Vednock, Theodore A
; APPLICANT: Pleiss, Michael A
; TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
; FILE REFERENCE: 123-US-CIPI
; CURRENT APPLICATION NUMBER: US/08/467,580B
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/273,055
; EARLIER FILING DATE: 1994-07-11
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 75
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: derived from VCAM-1
US-08-467-580-75

Query Match 60.0%; Score 21; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
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Db 2 PVSF 5
RESULT 4
PCT-US95-08516-75
; Sequence 75, Application PC/TUS9508516
; GENERAL INFORMATION:
; APPLICANT: ATHENA NEUROSCIENCES, INC.
; TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
; NUMBER OF SEQUENCES: 157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ATHENA NEUROSCIENCES, INC.
; STREET: 800 Gateway Blvd.
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08516
; FILING DATE: 10-JUL-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/273,055
; FILING DATE: 11-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 002010-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-3620
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-08516-75

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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
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Db 2 PVSF 5

RESULT 5
US-08-467-580-72
; Sequence 72, Application US/08467580B
; Patent No. 6001809
; GENERAL INFORMATION:
; APPLICANT: Thorsett, Eugene D
; APPLICANT: Vednock, Theodore A
; APPLICANT: Pleiss, Michael A
; TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
; FILE REFERENCE: 123-US-CIPI
; CURRENT APPLICATION NUMBER: US/08/467,580B
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/273,055
; EARLIER FILING DATE: 1994-07-11
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 72
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

GenCore version 5.1.6
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DM protein - protein search, using sw model

Run on: November 21, 2003, 15:27:54 ; Search time 6.71918 Seconds
(without alignments)
489.058 Million cell updates/sec

Title: US-09-010-377-5
Perfect score: 35
Sequence: 1 XXXXXXXPVFXXXXXX 18

Scoring table:
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Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	60.0	12	12	US-09-990-832C-103
3	21	60.0	13	14	US-10-010-310-3
4	21	60.0	13	14	US-10-010-310-6
5	21	60.0	14	10	US-09-982-172-88
6	21	60.0	14	10	US-09-982-172-224
7	21	60.0	14	11	US-09-880-748-3064
8	21	60.0	18	11	US-09-747-802-65
9	21	60.0	18	11	US-09-865-294-58
10	21	60.0	25	15	US-10-082-750-57
11	21	60.0	27	11	US-09-764-891-4315
12	21	60.0	32	9	US-09-864-761-34806
13	21	60.0	32	9	US-09-864-761-38915
14	21	60.0	33	15	US-10-144-929-92
15	21	60.0	35	10	US-09-764-877-1329

16	21	60.0	41	9	US-09-864-761-34763	Sequence 34763, A
17	21	60.0	42	9	US-09-864-761-42139	Sequence 42139, A
18	21	60.0	43	9	US-09-864-761-34242	Sequence 34242, A
19	21	60.0	43	12	US-10-029-386-33238	Sequence 33238, A
20	21	60.0	43	15	US-10-050-704-136	Sequence 136, App
21	21	60.0	43	15	US-10-062-548-122	Sequence 122, App
22	21	60.0	44	9	US-09-864-761-47048	Sequence 47048, A
23	21	60.0	44	9	US-09-864-761-47765	Sequence 47765, A
24	21	60.0	44	11	US-09-764-891-4075	Sequence 4075, App
25	21	60.0	45	9	US-09-864-761-44905	Sequence 44905, A
26	21	60.0	45	15	US-10-138-618-11	Sequence 11, Appl
27	21	60.0	46	12	US-09-933-767-1058	Sequence 1058, App
28	21	60.0	46	15	US-10-023-282-1058	Sequence 1058, App
29	21	60.0	47	11	US-09-764-891-2821	Sequence 2821, App
30	21	60.0	48	9	US-09-739-254-74	Sequence 74, Appl
31	21	60.0	48	9	US-09-904-615-74	Sequence 74, Appl
32	21	60.0	48	12	US-10-055-098-74	Sequence 74, Appl
33	21	60.0	48	12	US-10-029-386-31823	Sequence 31823, A
34	21	60.0	48	15	US-10-054-988-74	Sequence 74, Appl
35	21	60.0	49	9	US-09-764-878-112	Sequence 112, App
36	21	60.0	49	15	US-10-079-854-112	Sequence 112, App
37	21	60.0	50	9	US-09-864-761-45925	Sequence 45925, A
38	21	60.0	52	9	US-09-864-761-37265	Sequence 37265, A
39	21	60.0	52	9	US-09-864-761-47325	Sequence 47325, A
40	21	60.0	52	11	US-09-764-872-246	Sequence 246, App
41	21	60.0	53	9	US-09-864-761-46816	Sequence 46816, A
42	21	60.0	54	9	US-09-925-297-466	Sequence 466, App
43	21	60.0	54	12	US-10-012-952A-245	Sequence 245, App
44	21	60.0	60	11	US-09-764-891-5136	Sequence 5136, App
45	21	60.0	60	12	US-10-029-386-30343	Sequence 30343, A

ALIGNMENTS

RESULT 1
US-10-062-710-100
; Sequence 100, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qid, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV CTL-Epitopes
US-10-062-710-100

Query Match 60.0%; Score 21; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVSF 11

Db 1 PVSF 4

RESULT 2
US-09-990-832C-103
; Sequence 103, Application US/09990832C

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, Publication No. US20030149235A1
; GENERAL INFORMATION:
; APPLICANT: University Court of the University of Glasgow
; TITLE OF INVENTION: Targeting peptides
; FILE REFERENCE: PC/MC/JM/PI1910US
; CURRENT APPLICATION NUMBER: US/09/990,832C
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting peptide sequence
US-09-990-832C-103

Query Match 60.0%; Score 21; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
DB 6 PVSF 9

RESULT 3
US-10-010-310-3
; Sequence 3, Application US/10010310
; Publication No. US20020142348A1
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; APPLICANT: GEORGES, Elias
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING INTERACTING PROTEINS AND THE AMINO ACID
; FILE REFERENCE: 112418.122
; CURRENT APPLICATION NUMBER: US/10/010,310
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/134,259
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-310-3

Query Match 60.0%; Score 21; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
DB 1 PVSF 4

RESULT 4
US-10-010-310-6
; Sequence 6, Application US/10010310
; Publication No. US20020142348A1
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; APPLICANT: GEORGES, Elias
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING INTERACTING PROTEINS AND THE AMINO ACID
; FILE REFERENCE: 112418.122
; CURRENT APPLICATION NUMBER: US/10/010,310
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/134,259
; PRIOR FILING DATE: 1999-05-14
US-10-010-310-6

Query Match 60.0%; Score 21; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
DB 1 PVSF 4

US-10-010-310-6
; Publication No. US20030149235A1
; GENERAL INFORMATION:
; APPLICANT: University Court of the University of Glasgow
; TITLE OF INVENTION: Targeting peptides
; FILE REFERENCE: PC/MC/JM/PI1910US
; CURRENT APPLICATION NUMBER: US/09/990,832C
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting peptide sequence
US-09-990-832C-103

Query Match 60.0%; Score 21; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
DB 6 PVSF 9

RESULT 3
US-10-010-310-3
; Sequence 3, Application US/10010310
; Publication No. US20020142348A1
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; APPLICANT: GEORGES, Elias
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING INTERACTING PROTEINS AND THE AMINO ACID
; FILE REFERENCE: 112418.122
; CURRENT APPLICATION NUMBER: US/10/010,310
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/134,259
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-310-3

Query Match 60.0%; Score 21; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
DB 1 PVSF 4

RESULT 4
US-10-010-310-6
; Sequence 6, Application US/10010310
; Publication No. US20020142348A1
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; APPLICANT: GEORGES, Elias
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING INTERACTING PROTEINS AND THE AMINO ACID
; FILE REFERENCE: 112418.122
; CURRENT APPLICATION NUMBER: US/10/010,310
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/134,259
; PRIOR FILING DATE: 1999-05-14
US-10-010-310-6

Query Match 60.0%; Score 21; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
DB 1 PVSF 4

US-10-010-310-6
; Publication No. US20030149235A1
; GENERAL INFORMATION:
; APPLICANT: University Court of the University of Glasgow
; TITLE OF INVENTION: Targeting peptides
; FILE REFERENCE: PC/MC/JM/PI1910US
; CURRENT APPLICATION NUMBER: US/09/990,832C
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting peptide sequence
US-09-990-832C-103

Query Match 60.0%; Score 21; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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QY 8 PVSF 11
DB 6 PVSF 9

RESULT 3
US-10-010-310-3
; Sequence 3, Application US/10010310
; Publication No. US20020142348A1
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; APPLICANT: GEORGES, Elias
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING INTERACTING PROTEINS AND THE AMINO ACID
; FILE REFERENCE: 112418.122
; CURRENT APPLICATION NUMBER: US/10/010,310
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/134,259
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-310-3

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
DB 1 PVSF 4

RESULT 4
US-10-010-310-6
; Sequence 6, Application US/10010310
; Publication No. US20020142348A1
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; APPLICANT: GEORGES, Elias
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING INTERACTING PROTEINS AND THE AMINO ACID
; FILE REFERENCE: 112418.122
; CURRENT APPLICATION NUMBER: US/10/010,310
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/134,259
; PRIOR FILING DATE: 1999-05-14
US-10-010-310-6

Query Match 60.0%; Score 21; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
DB 1 PVSF 4

US-10-010-310-6
; Publication No. US20030149235A1
; GENERAL INFORMATION:
; APPLICANT: University Court of the University of Glasgow
; TITLE OF INVENTION: Targeting peptides
; FILE REFERENCE: PC/MC/JM/PI1910US
; CURRENT APPLICATION NUMBER: US/09/990,832C
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting peptide sequence
US-09-990-832C-103

Query Match 60.0%; Score 21; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
DB 6 PVSF 9

RESULT 3
US-10-010-310-3
; Sequence 3, Application US/10010310
; Publication No. US20020142348A1
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; APPLICANT: GEORGES, Elias
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING INTERACTING PROTEINS AND THE AMINO ACID
; FILE REFERENCE: 112418.122
; CURRENT APPLICATION NUMBER: US/10/010,310
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/134,259
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-310-3

Query Match 60.0%; Score 21; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
DB 9 PVSF 12

US-09-982-172-88
; Sequence 88, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATI
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-88

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
DB 9 PVSF 12

US-09-982-172-224
; Sequence 224, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATI
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 224
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-224

Query Match 60.0%; Score 21; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6
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M protein - protein search, using sw model

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473.510 Million cell updates/sec

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effect score: 35
sequence: 1 XXXXXXXXSVFXXXXXXX 18

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Gapop 10.0 , Gapext 0.5

searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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4	21	60.0	84	1 Y353_METJA	O06918 methanococ
5	21	60.0	88	1 YVAD_VACCC	P20513 vaccinia vi
6	21	60.0	96	1 ICTL_PIG	P15175 sus scrofa
7	21	60.0	99	1 YL30_ARCFU	Q28150 archaeglob
8	21	60.0	104	1 YBK0_YEAST	P38190 saccharomyc
9	21	60.0	107	1 LRF2_HSVIF	P17589 herpes simp
10	21	60.0	122	1 FOLB_CHLMU	Q9PJC6 chlamydia m
11	21	60.0	124	1 FOLB_CHLTR	O84620 chlamydia t
12	21	60.0	124	1 YBF3_YEAST	P38190 saccharomyc
13	21	60.0	125	1 OM10_RHILO	Q98h63 rhizobium 1
14	21	60.0	139	1 Y410_RHIME	Q52911 rhizobium m
15	21	60.0	141	1 RL11_LIBAS	P36250 liberibacte
16	21	60.0	144	1 INDC_BOVIN	P33046 bos taurus
17	21	60.0	144	1 YLX3_CAEEL	P46499 caenorhabdi
18	21	60.0	147	1 PG2_PIG	P32195 sus scrofa
19	21	60.0	147	1 R157_BOVIN	Q28183 bos taurus
20	21	60.0	147	1 Y720_SYNY3	P74650 synectocyst
21	21	60.0	149	1 FGI_PIG	P32194 sus scrofa
22	21	60.0	149	1 PG3_PIG	P32196 sus scrofa
23	21	60.0	149	1 PG4_PIG	P49933 sus scrofa
24	21	60.0	149	1 PG5_PIG	P49934 sus scrofa
25	21	60.0	149	1 YG2U_YEAST	P53263 saccharomyc
26	21	60.0	153	1 CORZ_COWRU	Q04302 cowdria rum
27	21	60.0	153	1 MP23_PIG	P49930 sus scrofa
28	21	60.0	153	1 R1B1_CAUCR	Q9A9S4 caulobacter
29	21	60.0	154	1 R1B8_CAMJE	Q9P1B9 campylobact
30	21	60.0	155	1 Y654_CHLPN	Q9Z7Q0 chlamydia p
31	21	60.0	156	1 R1S8_HELPJ	Q9Zn56 helicobacte
32	21	60.0	156	1 R1S8_HELPJ	O24854 helicobacte
33	21	60.0	158	1 MB27_BOVIN	P54228 bos taurus

34	21	60.0	159	1 MB28_BOVIN	P54229 bos taurus
35	21	60.0	160	1 SC53_SHEEP	P49928 ovis aries
36	21	60.0	160	1 SC53_SHEEP	P49929 ovis aries
37	21	60.0	163	1 TPX1_STRPN	P72500 streptococc
38	21	60.0	165	1 MB34_BOVIN	P56425 bos taurus
39	21	60.0	166	1 MP36_PIG	P49931 sus scrofa
40	21	60.0	167	1 MP37_PIG	P49932 sus scrofa
41	21	60.0	170	1 PA39_HUMAN	P49913 homo sapien
42	21	60.0	171	1 CP18_RABIT	P25230 oryctolagus
43	21	60.0	172	1 PR39_PIG	P80054 sus scrofa
44	21	60.0	174	1 FANG_ECOLI	P20861 escherichia
45	21	60.0	176	1 BCT5_BOVIN	P19660 bos taurus

ALIGNMENTS

RESULT 1

YOR3 TTV1
ID YOR3 TTV1 STANDARD; PRT; 57 AA.
AC P19278;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hypothetical 6.9 kDa protein.
OS Thermoproteus tenax virus 1 (strain KRAL) (TTV1).
OC Viruses; dsDNA viruses, no RNA stage; Lipothirixviridae;
OC Lipothirixvirus.
OX NCBI_TaxID=10480;
RN [1]
RP SEQUENCE FROM N.A.
RA Neumann H.;
RL Submitted (MAR-1989) to the EMBL/GenBank/DBJ databases.
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EMBL; X14855; CAA32971.1; -
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 57 AA; 6914 MW; B907370704263763 CRC64;

Query Match 60.0%; Score 21; DB 1; Length 57;
Best Local Similarity 100.0%; Pred.No. 61;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
D6 6 PVSF 9

RESULT 2

YAT1 RHOBL
ID YAT1 RHOBL STANDARD; PRT; 69 AA.
AC P05443;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last annotation update)
DE ATP synthase subunits region ORF 1 (Fragment).
OS Rhodopseudomonas blattica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1075;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85058188; PubMed=6209404;
RX Tybulewicz V L J., Falk G., Walker J.E.;
RA "Rhodopseudomonas blattica atp operon. Nucleotide sequence and
RT transcription.";

J. Mol. Biol. 179:185-214(1984).

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 EMBL; Z00018; CAA77307.1; -
 DR EMBL; Z00018; CAA77307.1; -
 DR PIR; S04666; S04666.
 DR Hypothetical protein.
 KW NON_TER 1
 FT SEQUENCE 69 AA; 7471 MW; 574EB0B6F8529ED9 CRC64;
 SQ SEQUENCE 69 AA; 7471 MW; 574EB0B6F8529ED9 CRC64;
 Query Match 60.0%; Score 21; DB 1; Length 69;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 PVSP 11
 Db 26 PVSP 29

RESULT 3
 RXL7 STAM STANDARD; PRT; 84 AA.
 AC Q53602; Q99W63;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative ribosomal protein L7Ae-like.
 GN SAV0544 OR SA0502 OR MW0499.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus (strain N315),
 OS Staphylococcus aureus (strain MW2), and
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878, 158879, 196620, 1280;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Mu50 / ATCC 700699, and N315;
 RC MEDLINE=213111952; PubMed=11418146;
 RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus."
 RL Lancet 357:1225-1240(2001).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Mu50 / ATCC 700699;
 RC MEDLINE=22040717; PubMed=12044378;
 RX Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.,
 RT "Genome and virulence determinants of high virulence community-acquired MRSA."
 RL Lancet 359:1819-1827(2002).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=NCCT 8325;
 RC MEDLINE=98241542; PubMed=95731165;
 RX Wada A., Watanabe H.,
 RA "Penicillin-binding protein 1 of Staphylococcus aureus is essential for growth."
 RT J. Bacteriol. 180:2759-2765(1998).
 RL J. Bacteriol. 180:2759-2765(1998).
 CC -!- SIMILARITY: BELONGS TO THE L7AE FAMILY OF RIBOSOMAL PROTEINS.

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 EMBL; AP003359; BAB56706.1; -
 DR EMBL; AP003359; BAB56706.1; -
 DR EMBL; AP004823; BAB94364.1; -
 DR EMBL; U20869; AAC46352.1; ALT_INIT.
 DR PIR; B89822; B89822.
 DR HAMAP; MF 00574; -; 1.
 DR InterPro; IPR002311; Ribosomal L30e.
 DR InterPro; IPR004038; Ribosomal L7A.
 DR InterPro; IPR004037; Ribosomal L7Ae.
 DR Pfam; PF01248; Ribosomal L7Ae; 1.
 DR Pfam; P801082; RIBOSOMAL L7AE; FALSE_NEG.
 DR KW Hypothetical protein; Ribosomal protein; Complete proteome.
 SQ SEQUENCE 84 AA; 9446 MW; 46EDC013ED029063 CRC64;
 Query Match 60.0%; Score 21; DB 1; Length 84;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 PVSP 11
 Db 57 PVSP 60

RESULT 4
 Y353 METJA STANDARD; PRT; 84 AA.
 ID Y353_METJA
 AC O06918;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ0353.
 GN MJ0353.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaeae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RC MEDLINE=96337999; PubMed=8688087;
 RX Bult C.J., White O., Olsen G.J., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Merrick J.M., Glodek A.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."
 RL Science 273:1058-1073(1996).
 CC
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 EMBL; U67488; AAB98342.1; -
 DR PIR; A64344; A64344.
 DR TIGR; MJ0353; -.
 KW Hypothetical protein; Complete proteome.

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PM protein - protein search, using sw model

Run on: November 21, 2003, 15:20:39 ; Search time 7.76712 Seconds
(without alignments)
598.027 Million cell updates/sec

Title: US-09-010-377-5
Perfect score: 35
Sequence: 1 XXXXXXXPVSFXXXXXX 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	60.0	34	Q96G86	Q96G86 homo sapien
2	21	60.0	35	Q9K016	Q9K016 neisseria m
3	21	60.0	36	Q8EYD2	Q8EYD2 leptospira
4	21	60.0	42	Q8FH25	Q8FH25 escherichia
5	21	60.0	45	P82989	P82989 desulfovibr
6	21	60.0	46	Q8U2K2	Q8U2K2 pyrococcus
7	21	60.0	47	Q9QWE3	Q9QWE3 rattus sp.
8	21	60.0	51	Q9IVV5	Q9IVV5 rotavirus a
9	21	60.0	51	Q9IVV9	Q9IVV9 rotavirus a
10	21	60.0	51	Q9IVV8	Q9IVV8 rotavirus a
11	21	60.0	51	Q9IVZ1	Q9IVZ1 rotavirus a
12	21	60.0	51	Q9IC28	Q9IC28 human rotav
13	21	60.0	51	Q9IVV7	Q9IVV7 rotavirus a
14	21	60.0	51	Q9IVV2	Q9IVV2 rotavirus a
15	21	60.0	51	Q9IVZ0	Q9IVZ0 rotavirus a
16	21	60.0	51	Q9IVV6	Q9IVV6 rotavirus a

17	21	60.0	53	4	Q9P1J0	Q9P1J0 homo sapien
18	21	60.0	54	6	Q8MJA2	Q8MJA2 macaca mula
19	21	60.0	60	2	Q93US8	Q93US8 carsonella
20	21	60.0	61	10	Q8GW73	Q8GW73 arabidopsis
21	21	60.0	61	16	Q8UGC9	Q8UGC9 agrobacteri
22	21	60.0	68	6	O77663	O77663 sus scrofa
23	21	60.0	69	6	Q8HXH4	Q8HXH4 macaca fasc
24	21	60.0	70	9	Q9FZU0	Q9FZU0 pseudomonas
25	21	60.0	71	2	Q8KYS1	Q8KYS1 bacillus an
26	21	60.0	76	2	Q47103	Q47103 escherichia
27	21	60.0	81	10	Q94D02	Q94D02 oryza sativ
28	21	60.0	81	10	Q8LMD4	Q8LMD4 oryza sativ
29	21	60.0	81	16	Q92RL4	Q92RL4 rhizobium m
30	21	60.0	84	9	Q9G066	Q9G066 bacterioph
31	21	60.0	84	16	Q98R37	Q98R37 rhizobium l
32	21	60.0	84	17	Q8TQ71	Q8TQ71 methanosarc
33	21	60.0	86	10	Q9SKP3	Q9SKP3 arabidopsis
34	21	60.0	86	10	Q8L9D5	Q8L9D5 arabidopsis
35	21	60.0	86	16	Q8CTS9	Q8CTS9 straphylecoc
36	21	60.0	87	2	O52175	O52175 salmonella
37	21	60.0	88	12	Q9JF92	Q9JF92 vaccinia vi
38	21	60.0	89	16	Q98HK4	Q98HK4 rhizobium l
39	21	60.0	91	2	Q9L5F8	Q9L5F8 salmonella
40	21	60.0	92	16	Q935W7	Q935W7 salmonella
41	21	60.0	93	3	Q96TS3	Q96TS3 schizophyll
42	21	60.0	93	16	Q97HM7	Q97HM7 clostridium
43	21	60.0	94	12	Q9DJ76	Q9DJ76 foot-and-mo
44	21	60.0	95	16	Q8FID2	Q8FID2 escherichia
45	21	60.0	96	2	Q9RLG9	Q9RLG9 enterococcu

ALIGNMENTS

RESULT 1

Q96G86 PRELIMINARY; PRT; 34 AA.
 ID Q96G86;
 AC Q96G86;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009886; AAH09886.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 34 AA; 3602 MW; 4C7FCC8FE67094B7 CRC64;

Query Match 60.0%; Score 21; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVSF 11

Db 7 PVSF 10

RESULT 2

Q9K016 PRELIMINARY; PRT; 35 AA.
 ID Q9K016;
 AC Q9K016;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein NMS0613.
 GN NMS0613.

OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / Serogroup B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 Eisen J.A., Ketchum K.A., Hood D.W., Feden J.F., Dodson R.J.,
 Nelson W.C., Gunn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 Mason T., Ciecko A., Parksey D.S., Blair E., Citron H., Clark E.B.,
 Cotton M.D., Urtterback T.R., Khouri H., Qin H., Vamathevan J.,
 Gill J., Searlato V., Masignani V., Pizza M., Grandi G., Sun L.,
 Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58";
 RL Science 287:1809-1815(2000).
 DR EMBL; AE002416; AAF41040.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 35 AA; 4022 MW; A3677246569B6306 CRC64;

Query Match 60.0%; Score 21; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
 Db 21 PVSF 24

RESULT 3
 Q8EYD2 PRELIMINARY; PRT; 36 AA.
 ID Q8EYD2
 AC Q8EYD2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Hypothetical protein.
 GN LA4284.
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB011582; AAN51482.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 36 AA; 4349 MW; 1568528D23C536D5 CRC64;

Query Match 60.0%; Score 21; DB 16; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
 Db 21 PVSF 24

RESULT 4
 Q8FH25 PRELIMINARY; PRT; 42 AA.
 ID Q8FH25
 AC Q8FH25;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Hypothetical protein.
 GN C2108.
 OS Escherichia coli O6.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=124711157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; AB016761; AAN80568.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 42 AA; 4552 MW; 7A6C730612538776 CRC64;

Query Match 60.0%; Score 21; DB 16; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
 Db 27 PVSF 30

RESULT 5
 P82989 PRELIMINARY; PRT; 45 AA.
 ID P82989
 AC P82989;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Cytochrome c3 (Fragment).
 OS Desulfovibrio africanus.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=873;
 RN [1]

RP SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, AND HEME-BINDING.
 RC STRAIN=NCIB 8401 / BENGHAZI;
 RX MEDLINE=96162885; PubMed=8573595;
 RA Pieulle L., Haladjian J., Bonicel J., Hatchikian E.C.;
 RT "Biochemical studies of the c-type cytochromes of the sulfate reducer
 Desulfovibrio africanus. Characterization of two tetraheme cytochromes
 c3 with different specificity";
 RL Biochim. Biophys. Acta 1273:51-61(1996).
 CC -!- FUNCTION: EXCHANGES ELECTRONS WITH [NIFE] HYDROGENASES.
 CC PARTICIPATES IN SULFATE RESPIRATION COUPLED WITH PHOSPHORYLATION
 CC BY TRANSFERRING ELECTRONS FROM THE ENZYME DEHYDROGENASE TO
 CC FERREDOXIN.

CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: PERIPLASMIC (BY SIMILARITY).

CC -!- PTM: BINDS 8 HEMES.

CC -!- MISCELLANEOUS: ACIDIC TETRAHEME C3 IS NOT A SUBUNIT OF THIS
 CC OCTAHEME CYTOCHROME C3.

DR InterPro; IPR000345; Cyt c heme bind.

DR PROSITE; PS00190; CYTOCHROME C; PARTIAL.

KW Electron transport; Sulfate respiration; Heme; Periplasmic.

FT METAL 42 42 IRON (HEME 1 AXIAL LIGAND).

FT METAL 45 45 IRON (HEME 3 AXIAL LIGAND).

FT NON_TER 45 45

SQ SEQUENCE 45 AA; 5114 MW; 1A67207235DD4DB4 CRC64;

Query Match 60.0%; Score 21; DB 2; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVSF 11
 Db 19 PVSF 22